AMENDMENTS TO THE SPECIFICATION

Please amend the specification as described below.

Delete paragraphs 0058-0096.

Replace paragraph 0155 with the following paragraph.

> The nucleotide sequences of each of a plurality of GAM oligonucleotides that are described by Fig. 1 and their respective genomic sources and genomic locations are set forth in Tables 1-3, hereby incorporated herein. Specifically, in Table 1, line 778 describes GAM RNA (miRNA) as set forth in SEQ ID NO: 348 is shown as predicted from human.

After paragraph 0155, add the following Table 1, paragraph, Table 2, paragraph, and Table 3.

Table 1

GAM SEQ-ID	GAM NAME	GAM RNA SEQUENCE	GAM ORGANISM	GAM POS
348	GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	A

> In Table 2, lines 42112-42207, describes GAM PRECURSOR RNA (hairpin) as set forth in SEQ ID NO: 4233864 and as it relates to Figures 1-8 .

Table 2

GAM NAME	GAM ORGANISM	PRECUR SEQ-ID	PRECURSOR SEQUENCE	GAM DESCRIPTION
GAM 353678	Human	4233864	CCTGCTCCCG CCCCAGCAGC ACACTGTGGT TTGTACGGCA CTGTGGCCAC GTCCAAACCA CACTGTGGTG TTAGAGCGAG GGTGGGGGAGG	Fig. 1 further provides a conceptual description of another novel bioinformatically-detected human oligonucleotide of the present invention referred to here as the Genomic Address Messenger 353678 (GAM353678) oligonucleotide, which modulates expression of respective target genes whose function and utility are known in the art. GAM353678 is a novel bioinformatically detectable regulatory, non-

protein-coding, miRNA-like oligonucleotide. The method by which GAM353678 is detected is described with additional reference to Figs. 1-8. The GAM353678 precursor, herein designated GAM PRECURSOR, is encoded by the Human genome. GAM353678 target gene, herein designated GAM TARGET GENE, is a target gene encoded by the target organism as specified in Tables 6-7. The GAM353678 precursor, herein designated GAM PRECURSOR, encodes a GAM353678 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA oligonucleotides, the GAM353678 precursor RNA does not encode a protein. GAM353678 precursor RNA folds onto itself, forming GAM353678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional "hairpin" structure. GAM PRECURSOR RNA folds onto itself, forming GAM FOLDED PRECURSOR RNA, which has a two-dimensional "hairpin structure". As is well-known in the art, this "hairpin structure" is typical of RNA encoded by known miRNA precursor oligonucleotides and is due to the full or partial complementarity of the nucleotide sequence of the first half of an miRNA precursor to theRNA that is encoded by a miRNA oligonucleotide to the nucleotide sequence of the second half thereof. A nucleotide sequence that is identical or highly similar to the nucleotide sequence of the GAM353678 precursor RNA is designated SEQ ID NO:4233864, and is provided hereinbelow with reference to the sequence listing section. The nucleotide sequence designated SEQ ID NO:4233864 is located from position 7121806 to position 7121896 relative to chromosome 17 on the "-" strand, and overlaps an intergenic region (UCSC.h16.refGene database). Furthermore, the nucleotide sequence designated SEQ ID NO:4233864 is positioned in a region that is conserved

between human, mouse and rat (UCSC.hg16.humorMm3Rn3). A schematic representation of a predicted secondary folding of GAM353678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA is set forth in Table 4 incorporated herein. An enzyme complex designated DICER COMPLEX, an enzyme complex composed of Dicer RNaseIII together with other necessary proteins, cuts the GAM353678 folded precursor RNA yielding a single-stranded ~22 nt-long RNA segment designated GAM353678 RNA, herein designated GAM RNA.Table 5 provides a nucleotide sequence that is highly likely to be identical or extremely similar to the nucleotide sequence of GAM353678 RNA, hereby incorporated herein. GAM353678 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, designated GAM353678 target RNA, herein designated GAM TARGET RNA. As is typical of mRNA of a protein-coding gene, GAM353678 target RNA comprises three regions, as is typical of mRNA of a protein-coding gene: a 5' untranslated region, a protein-coding region and a 3' untranslated region, designated 5'UTR, PROTEIN-CODING and 3'UTR, respectively. GAM353678 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in the untranslated regions of GAM353678 target RNA. This complementary binding is due to the partial or full complementarity between the nucleotide sequence of GAM353678 RNA and the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 1 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III, respectively. It is appreciated that the number of target binding sites shown in Fig. 1 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig.

1 shows target binding sites only in the 3'UTR region, these target binding sites may instead be located in the 5'UTR region or in both the 3'UTR and 5'UTR regions. The complementary binding of GAM353678 RNA, herein designated GAM RNA, to target binding sites on GAM353678 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits the translation of GAM353678 target RNA into respective GAM353678 target protein, herein designated GAM TARGET PROTEIN, shown surrounded by a broken line. It is appreciated that the GAM353678 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM353678 target genes. The mRNA of each one of this plurality of GAM353678 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM353678 RNA, herein designated GAM RNA, and which when bound by GAM353678 RNA causes inhibition of translation of the GAM353678 target mRNA into a corresponding GAM353678 target protein. The mechanism of the translational inhibition that is exerted by GAM353678 RNA, herein designated GAM RNA, on one or more GAM353678 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted by known miRNA oligonucleotides. The nucleotide sequence of GAM353678 precursor RNA, herein designated GAM PRECURSOR RNA, its respective genomic source and genomic location and a schematic representation of a predicted secondary folding of GAM353678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA are set forth in Tables 3-4, hereby incorporated herein. The nucleotide sequences of a "diced" GAM353678 RNA, herein

designated GAM RNA, from GAM353678 folded precursor RNA are set forth in Table 5, hereby incorporated herein. The nucleotide sequences of target binding sites, such as BINDING SITE I, BINDING SITE II and BINDING SITE III of Fig. 1, found on GAM353678 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM353678 RNA, herein designated GAM RNA, are set forth in Tables 6-7, hereby incorporated herein. It is appreciated that the specific functions and accordingly the utilities of GAM353678 RNA are correlated with and may be deduced from the identity of the GAM353678 target gene inhibited thereby, and whose functions are set forth in Table 8, hereby incorporated herein.

Table 3, lines 1279-1280, shows data relating to the source and location of the GAM oligonucleotide, specificaly the GAM PRECRSOR (hairpin) and its position in the genomic sequence of human.

Table 3

GAM NAME	PRECURSOR SEQ-ID	GAM ORGANISM	SOURCE	STRAND	SRC-START OFFSET	SRC-END OFFSET
GAM353678	4233864	Human	17		7121806	7121896

Replace paragraph 0156 with the following paragraph.

The nucleotide sequences of GAM PRECURSOR RNAs, and a schematic representation of a predicted secondary folding of GAM FOLDED PRECURSOR RNAs, of each of a plurality of GAM oligonucleotides described by Fig. 1 are set forth in Table 4, hereby incorporated herein. Table 4 lines 2384-2388, shows a schematic representation of the GAM folder precursor as set forth in SEQ ID NO:348 , beginning at the 5' end (beginning of upper row) to the 3'

end (beginning of lower row), where the hairpin loop is positioned at the right part of the drawing.

After paragraph 0156, add the following Table 4.

Table 4

GAM NAME	PRE CUR SEQ -ID	GAM ORGANISM	PRECURSOR SEQUENCE	GAM FOLDED PRECURSOR RNA
GAM353678	423	Human	CCTGCTCCCGCCCCAGCAGC	G C------ G C T -- AC
	386			
	4		ACACTGTGGTTTGTACGGCA	CCT CTCCCGCCC AGCA CACA TGTGGTTTG AC GGC T
			CTGTGGCCACGTCCAAACCA	GGA GGGGGTGGG TTGT GTGT ACACCAAAC TG CCG G
			CACTGTGGTGTTAGAGCGAG	- AGCGAGA G C C CA GT
			GGTGGGGGAGG	

Replace paragraph 0157 with the following paragraph.

The nucleotide sequences of "diced" GAM RNAs of each of a plurality of GAM oligonucleotides described by Fig. 1 are set forth in Table 5, hereby incorporated herein. Table 5 , line 1276 shows the mature GAM RNA as set forth in SEQ ID NO: 348 as sliced by DICER from the GAM PRECURSOR sequence (hairpin) as set forth in SEQ ID NO: 4233864.

After paragraph 0157, add the following Table 5.

GAM NAME	GAM ORGANISM	GAM RNA SEQUENCE	PRECUR SEQ-ID	GAM POS
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	4233864	A

Replace paragraph 0158 with the following paragraph.

The nucleotide sequences of target binding sites, such as BINDING SITE I, BINDING SITE II and BINDING SITE III that are found on GAM TARGET RNAs of each of a plurality of GAM oligonucleotides that are described by Fig. 1, and a schematic representation of the complementarity of each of these Target binding sites to each of a plurality of GAM RNAs that are described by Fig. 1 are set forth in Tables 6-7, hereby incorporated herein. Table 6 shows data relating to the SEQ ID NO of the GAM target binding site sequence of the target gene name as bound by the GAM RNA as set forth in SEQ ID NO: 348. Table 6, lines 3688165, 767082, 762322 and 763042 related to target binding site SEQ ID NO: 1810388, 673420, 671402 respectively.

After paragraph 0158, add the following Table 6, paragraph, and Table 7.

Table 6

TARGET BINDING SITE SEQ-ID	TARGET ORGANISM	TARGET	TARGET BINDING SITE SEQUENCE
1810388	Human	MGAT5	CACCATGCTGCTG
673420	Human	SERPINH1	AAACTAGGTGCTGCAG
671402	Human	SERPINH1	ATACCATGATGCTG
671042	Human	SERPINH1	CTATAAAACTAGGTGCTGCAG

Table 7, lines 312839-313773 shows data relating to target genes and binding site of GAM oligonucleotides.

Table 7

GAM NAME	GAM ORGANISM	GAM RNA SEQUENCE	TARGET BS-SEQ	TARGET	TARGET REF-ID	TARGET ORGANISM	UTR	BINDING SITE DRAW (UPPER:TARGET;LOWER:GAM)	GAM POS
GAM353678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACCAAA CTTATGCA GCTG	nupC	NC_004431 from 2795390 to 2796631 (+)	Escherichia coli CFT073	3	--- A C TA A AAACCA A T TGC GCTG TTTGGT T A ACG CGAC ATG G C C- A	A
GAM353678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACCAAA CTTATGCA GCTG	nupC	NC_004741 from 2494019 to 2495221 (+)	Shigella flexneri 2a str. 2457T	3	--- A C TA A AAACCA A T TGC GCTG TTTGGT T A ACG CGAC ATG G C C- A	A
GAM353678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACCCTG CTGCG	relA	NC_000962 from 2907824 to 2910196 (-)	Mycobacteriu m tuberculos is H37Rv	3	--- C----- - AAACC TGCTGC G TTTGG ACGACG C ATG TGTCAC A	A

GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACCCTGCTGCG	relA	NC_002945 from 2875274 to 2877646 (-)	Mycobacteriu m bovis subs p bovis AF2122/97	3	ATG	---C-----TGTCAC	-AAACCTTTGGACGACGCA
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACCCTTTCTGCTGCTT	yabO	NC_004431 from 61489 to 62148 (-)	Escherichia coli CFT073	3	ATG	---C TTC-T TCAC	AAAACC TTGCTGCTTTGG GACGACGAC
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACCGATGCAGTGCGGCTG	amtB	NC_004337 from 4080595 to 4093405 (+)	Shigella flexneri 2a str. 301	3	ATG	---AT CAG GGT AC-	GAAACCG GTTGGT CACG CGAA
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACCGATGCAGTGCGGCTG	amtB	NC_004741 from 4078606 to 4091466 (+)	Shigella flexneri 2a str. 2457T	3	ATG	---AT CAG GGT AC-	GAAACCG GTTGGT CACG CGAA
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACCGATGCCGTGCGGCTG	amtB	NC_004431 from 5476162 to 5489002 (+)	Escherichia coli CFT073	3	ATG	---AT CCG GGT AC-	GAAACCG GTTGGT CACG CGAA
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACCGCCCCCAGTCTGCTG	dsdA	NC_003197 from 4004453 to 4005775 (+)	Salmonella typhimurium LT2	3	CTGCTG	---CCCCAG -AAACCGC T TTTGGTG A GACGAC ATG TCAC-- C	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACCGGCCTTGCCGCTG	gadA	NC_002947 from 4871625 to 4872929 (+)	Pseudomonas putida KT2440	3	ATG	---GCC - C AAACCG T TGC GCTG TTTGGT A ACG CGAC GTC C A	
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACGAATTGAATCATGCCGCTG	aroA	NC_003116 from 1557502 to 1558803 (+)	Neisseria meningitidis Z2491	3	GCTG	---G ATTGAATCA C AAAC A TGC A TTTG T ACG CGAC ATG G GTCAC---- A	
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACGACGGGCTGCTG	ruvB	NC_003143 from 2336449 to 2337453 (+)	Yersinia pestis	3	ACG TGT CACA	---G ---G AAAC GCTGCTG TTTG CGACGAC ATG G	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACGACGGGCTGCTG	ruvB	NC_004088 from 2482031 to 2483035 (-)	Yersinia pestis KIM	3	ACG TGT CACA	---G ---G AAAC GCTGCTG TTTG CGACGAC ATG G	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACGATATCCTGCTG	yciE	NC_004431 from 1558641 to 1559147 (-)	Escherichia coli CFT073	3	ATG	---G --- C AAAC ATA T CTGCTG TTTG TGT A GACGAC G CAC C	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAACGCATGTTCATGCGCTG	vanB	NC_002516 from 5504120 to 5505073 (+)	Pseudomonas aeruginosa PA01	3	GCTG ACG C-	---G T CA - AAAC CATG T TGC A TTTG GTGT A CGAC ATG - C A	
GAM3536 78	Human	CAGCAGCACACTGTGG	AAACGCTCCGTATACT	ftsY	NC_000922 from 1115454	Chlamydophil a	3	---A	GC CCGTATAC A AAAC T	

		TTTGTA	GCTGCTA		27 to 11162 99 (-)	pneumoniae CWL029		TGCTGCT TTTG G ACGACGA ATG GT TCAC---- C		
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACGCTC CGTATACT GCTGCTA	ftsY	NC_002491 from 11131 27 to 11139 99 (-)	Chlamydophila pneumoniae J138	3	--- GC CCGTATAC A AAAC T TGCTGCT TTTG G ACGACGA ATG GT TCAC---- C		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACTAAT CGACAGTT GCTGCG	rbsR	NC_004337 from 39477 08 to 39487 00 (+)	Shigella flexneri 2a str. 301	3	--- ATCGACAGT - AAACTA TGCTGC G TTTGGT ACGACG C ATG GTCAC---- A		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACTAAT CGACAGTT GCTGCG	rbsR	NC_004741 from 38245 94 to 38255 77 (-)	Shigella flexneri 2a str. 2457T	3	--- ATCGACAGT - AAACTA TGCTGC G TTTGGT ACGACG C ATG GTCAC---- A		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACTAGG TGCTGCAG	SERPINH 1	NM_001235	Human	3	--- G --- A AAACTA G TGCTGC G TTTGGT T ACGACG C ATG G CAC A		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AAACTCAG GCTGGCAA GCTGCTG	aroH	NC_004337 from 15575 27 to 15585 73 (-)	Shigella flexneri 2a str. 301	3	--- T G C GCAA AAAC CA G TG GCTGCTG TTTG GT T AC CGACGAC ATG - G C ---A		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AAAGCTGC TGCTT	zraP	NC_003197 from 43877 27 to 43881 82 (-)	Salmonella typhimurium LT2	3	--- G ------ T AAA C TGCTGCT TTT G ACGACGA ATG G TGTCAC C		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AAATCAGT TGTACTTG TTGCTG	cysM	NC_003197 from 25516 51 to 25525 62 (-)	Salmonella typhimurium LT2	3	--- GTTGTACT T AAATCA TG TGCTG TTTGGT AC ACGAC ATG GTCAC--- G		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AACATTGC TGCTG	rbsR	NC_004431 from 44392 60 to 44402 52 (+)	Escherichia coli CFT073	3	--- - - ---- AA C AT TGCTGCTG TT G TG ACGACGAC ATG T G TCAC		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AACTGCTG CTC	oxyR	NC_003197 from 43430 80 to 43439 97 (+)	Salmonella typhimurium LT2	3	--- - ------- C AA C TGCTGCT TT G ACGACGA ATG T GTGTCAC C		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AACTGCTG CTC	oxyR	NC_003198 from 36072 04 to 36081 21 (-)	Salmonella enterica enterica serovar Typhi	3	--- - ------- C AA C TGCTGCT TT G ACGACGA ATG T GTGTCAC C		A
GAM3678	Human	CAGCAGCA CACTGTGG TTTGTA	AACTGCTG CTC	oxyR	NC_004631 from 35928 64 to 35937 81 (-)	Salmonella enterica enterica serovar	3	--- - ------- C AA C TGCTGCT TT G ACGACGA ATG T GTGTCAC C		A

						Typhi Ty2				
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AAGCCGGTTGCGGTGCTGCTG	aroA	NC_003116 from 1557502 to 1558803 (+)	Neisseria meningitidis Z2491	3	--- AAGCCG TTTGGT	GTTGCGG TGCTGCTG ACGACGAC ATG GTCAC--	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AATCCACTCCGTGTTGCTG	glgP	NC_003198 from 4144568 to 4147015 (+)	Salmonella enterica enterica serovar Typhi	3	--- CCAC GGTG	T TCC T AA GTG TGCTG TT CAC ACGAC ATG T TCA G	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	AATCCACTCCGTGTTGCTG	glgP	NC_004631 from 4129215 to 4131662 (+)	Salmonella enterica enterica serovar Typhi Ty2	3	--- CCAC GGTG	T TCC T AA GTG TGCTG TT CAC ACGAC ATG T TCA G	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	ACATGCTGCTT	nupC	NC_004431 from 2795390 to 2796631 (+)	Escherichia coli CFT073	3	--- A T ATG	-- - ----- C A TGCTGCT T G T ACGACGA TT G GTCAC T C	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	ACATGCTGCTT	nupC	NC_004741 from 2494019 to 2495221 (+)	Shigella flexneri 2a str. 2457T	3	--- A T ATG	-- - ----- C A TGCTGCT T G T ACGACGA TT G GTCAC T C	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	ACGATGGTGTACTGCTGCTT	phoY2	NC_000962 from 913556 to 914197 (-)	Mycobacterium tuberculosis H37Rv	3	--- TGTCAC G	-- G T TGCTGCT ACGACGA G ---	TAC A C ATGGTG T G ATG TT C	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	ACGATGGTGTACTGCTGCTT	phoY2	NC_002945 from 914388 to 915029 (-)	Mycobacterium bovis subsp bovis AF2122/97	3	--- TGTCAC G	-- G T TGCTGCT ACGACGA G ---	TAC A C ATGGTG T G ATG TT C	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	ACTGCTGCTC	glgP	NC_003198 from 4144568 to 4147015 (+)	Salmonella enterica enterica serovar Typhi	3	--- A T ATG	-- ------- C C TGCTGCT G ACGACGA TT GTGTCAC C	A
GAM3536 78	Human	CAGCAGCACACTGTGGTTTGTA	ACTGCTGCTC	glgP	NC_004631 from 4129215 to 4131662 (+)	Salmonella enterica enterica serovar Typhi Ty2	3	--- A T ATG	-- ------- C C TGCTGCT G ACGACGA TT GTGTCAC C	A
GAM3536 78	Human	CAGCAGCACACTGTGG	AGAATGTTGTTAGTGC	recG	NC_002677 from 2014	Mycobacterium m	3	--- AGA	-- T TTAG ATG TG	A

		TTTGTA	TGCTG		23 to 20169 54 (-)	leprae		TGCTGCTG TTT TGT AC ACGACGAC ATG GG C ----		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	AGACCATG AAGAACTG GCTGCTG	relA	NC_000962 from 29078 24 to 29101 96 (-)	Mycobacteriu m tuberculos is H37Rv	3	--- AA AACTG AGACCATG G A GCTGCTG TTTGGTGT C CGACGAC ATG CA ----A		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	AGACCATG AAGAACTG GCTGCTG	relA	NC_002945 from 28752 74 to 28776 46 (-)	Mycobacteriu m bovis subs p bovis AF21 22/97	3	--- AA AACTG AGACCATG G A GCTGCTG TTTGGTGT C CGACGAC ATG CA ----A		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	AGCTTGCT GCTG	glpC	NC_003143 from 42896 50 to 42908 97 (-)	Yersinia pestis	3	--- - ------ AG CT A TGCTGCTG TT GG ACGACGAC ATG T TGTCAC		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	AGCTTGCT GCTG	glpC	NC_004088 from 4546 77 to 45604 7 (+)	Yersinia pestis KIM	3	--- - ------ AG CT A TGCTGCTG TT GG ACGACGAC ATG T TGTCAC		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	ATACCAAG GCTGCTG	ftsY	NC_000922 from 11154 27 to 11162 99 (-)	Chlamydophila pneumoniae CWL029	3	--- T A----G A ACCA GCTGCTG T A TGGT CGACGAC ATG T GTCACA		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	ATACCAAG GCTGCTG	ftsY	NC_002491 from 11131 27 to 11139 99 (-)	Chlamydophila pneumoniae J138	3	--- T A----G A ACCA GCTGCTG T A TGGT CGACGAC ATG T GTCACA		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	ATACCATG ATGCTG	SERPINH 1	NM_001235	Human	3	--- T ----- A A ACCA TG TGCTG T A TGGT AC ACGAC ATG T GTCAC G		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	ATTTCTGC TGCTT	aroD	NC_004342 from 481 28 to 48832 (-)	Leptospira interrogans serovar lai str. 56601	3	--- TT ------ T A A TC TGCTGCT T GG ACGACGA ATG TT TGTCAC C		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAAAACG GTCTGCCG CTG	accC	NC_002929 from 9264 07 to 92777 7 (+)	Bordetella pertussis	3	-- A- C C A CAAA ACGGT TGC GCTG GTTT TGTCA ACG CGAC AT GG C A		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAAAGCT TTTCGCTT GCGGCTG	zraP	NC_003197 from 43877 27 to 43881 82 (-)	Salmonella typhimurium LT2	3	-- -- GCT TTCGCT G CAAA A T TGC A GCTG GTTT T A ACG CGAC AT GG GTC C----- A		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAAAGTC GTCCTGTG CGGCTG	glpD	NC_004310 from 2107 63 to 21227 4 (+)	Brucella suis 1330	3	-- -- GTCGTCCTG G CAAA A TGC A GCTG GTTT T ACG CGAC AT GG GTCAC---- A		
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAACAGG CTGCTGCT G	avtA	NC_004337 from 37211 75 to 37225	Shigella flexneri	3	-- - G C-- CAAAC A A G TGCTGCTG GTTTG T T ACGACGAC AT G		

					33 (+)	2a str. 301		G CAC			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAACAGG CTGCTGCT G	avt A	NC_004741 from 4052685 to 4053938 (-)	Shigella flexneri 2a str. 2457T	3	-- A G T T G C-- A G T G C A C	- TGCTGCTG ACGACGAC	CAAAC GTTTG AT G	A
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAACATC ATGGTTGC TGTTG	mia A	NC_000117 from 899276 to 900295 (+)	Chlamydia trachomatis	3	-- TG A	- CA GT CAAAC AT TG TGCTG GTTTG TG AC ACGAC AC AT G TC -- G	T A	
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAACCAG CGGTCTGC TG	selB	NC_002947 from 582133 to 584055 (+)	Pseudomonas putida KT244 0	3	-- AT	GC G- - CAAACCA G T CTGCTG GTTTGGT C A GACGAC GT AC C	A	
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAACCAT GATGCTG	mia A	NC_000117 from 899276 to 900295 (+)	Chlamydia trachomatis	3	-- AT	----- A CAAACCA TG TGCTG GTTTGGT AC ACGAC GTCAC G	A	
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAACCGA CCCTGCTG CTG	minE	NC_002947 from 193268 to 193294 (-)	Pseudomonas putida KT244 0	3	-- AT	ACCC- CAAACCG TGCTGCTG GTTTGGT ACGACGAC GTCAC	A	
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAACCGC AGTACTGG TGCTG	dnaE	NC_002677 from 142301 to 142654 (+)	Mycobacterium leprae	3	-- AT	AC G CAAACCGCAGT TG TGCTG GTTTGGTGTCA AC ACGAC C- G	A	
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAACTCT TTTTCTTC TGCTG	aroD	NC_004342 from 481 to 488322 (-)	Leptospira interrogans serovar lai str. 56601	3	-- AT	C TT TC T CAAACT T T T CTGCTG GTTTGG G A A GACGAC T TC C- C	A	
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAAGCAC TGCTGCTG	ptsH	NC_003198 from 2505403 to 2505660 (+)	Salmonella enterica enterica serovar Typhi	3	-- CAC GTG	G ---- TGCTGCTG ACGACGAC AT TCAC	CAAA GTTT G	A
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAAGCCG CGTGCGCT G	amtB	NC_004337 from 40805 to 40934 (+)	Shigella flexneri 2a str. 301	3	-- AT	G CGC -- - CAAA C G TGC GCTG GTTT G C ACG CGAC G TGT AC A	A	
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAAGCCG CGTGCGCT G	amtB	NC_004431 from 54761 to 54890 (+)	Escherichia coli CFT073	3	-- AT	G CGC -- - CAAA C G TGC GCTG GTTT G C ACG CGAC G TGT AC A	A	
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CAAAGCCG CGTGCGCT G	amtB	NC_004741 from 40786 to 40914 (+)	Shigella flexneri 2a str. 2457T	3	-- AT	G CGC -- - CAAA C G TGC GCTG GTTT G C ACG CGAC G TGT AC A	A	
GAM35 3678	Human	CAGCAGCA	CAAAGCCT	pil	NC_002947 from	Pseudom	3	--	G C TT TTCGG		A

3678	an	CACTGTGG TTTGTA	TTTTTCGG GCTGCTG	T	rom 34 to 44	58169 58179 (-)	onas putida KT244 0	CAAA C T T GCTGCTG GTTT G G A CGACGAC AT G T TC C---A	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAAAGCGT CATGTAAT GCTTGCTG	cys M	NC_003197 rom 51 to 62	25516 25525 (-)	Salmone lla t yphimur ium L T2	3 -- G CA TAA T CAAA CGT TG TGCT A GCTG GTTT GTG AC ACGA CGAC AT G TC --- -	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAAATCCC CAGTTGTG CTG	glc C	NC_004431 rom 71 to 95	35428 35436 (+)	Escheri chia coli CFT073	3 -- C CAGT - CAAATC C TG TGCTG GTTTGG G AC ACGAC AT T TCAC G	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAACACAT TACTGCTT GCTCTG	aro H	NC_004337 rom 27 to 73	15575 15585 (-)	Shigell a fle xneri 2a str . 301	3 -- CA TACTGCT - CAA CAT TGCT A CTG GTT GTG ACGA GAC AT TG TCAC--- C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAACACTT TGCGCTG	spe D	NC_003197 rom 01 to 5	1942 19499 (-)	Salmone lla t yphimur ium L T2	3 -- - - TT-- - CAA C AC TGC GCTG GTT G TG ACG CGAC AT T G TCAC A	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAACACTT TGCGCTG	spe D	NC_003198 rom 89 to 3	1963 19718 (-)	Salmone lla e nterica ente rica serovar Typhi	3 -- - - TT-- - CAA C AC TGC GCTG GTT G TG ACG CGAC AT T G TCAC A	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAACACTT TGCGCTG	spe D	NC_004631 rom 80 to 4	1963 19717 (-)	Salmone lla e nterica ente rica serovar Typhi Ty2	3 -- - - TT-- - CAA C AC TGC GCTG GTT G TG ACG CGAC AT T G TCAC A	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAACAGCA GTTGCTGC TG	ace K	NC_002947 rom 42 to 57	51847 51864 (-)	Pseudom onas putida KT244 0	3 -- - - GCAGT CAA C A TGCTGCTG GTT G T ACGACGAC AT T G GTCAC	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAACAGTT TCTTGGTC TGCTG	fmt B(m r p)	NC_002745 rom 45 to 90	22181 22255 (-)	Staphyl ococc us aureus su bsp. aureus N315	3 -- - - GTT CTTGG - CAA C A T T A CTGCTG GTT G T A A GACGAC AT T G GTC C---- C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAACAGTT TCTTGGTC TGCTG	fmt B(m r p)	NC_002758 rom 35 to 80	22879 22953 (-)	Staphyl ococc us aureus su bsp. aureus Mu50	3 -- - - GTT CTTGG - CAA C A T T A CTGCTG GTT G T A A GACGAC AT T G GTC C---- C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAACAGTT TCTTGGTC TGCTG	tru nca t ed fmt	NC_003923 rom 83 to 43	22380 22401 (-)	Staphyl ococc us aureus su bsp.	3 -- - - GTT CTTGG - CAA C A T T A CTGCTG GTT G T A A GACGAC AT T G GTC C---- C	

				B			aureus MW2			
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACCCAC CAGCACTG CTGCG	cysQ	NC_002947 from 315184 to 315984	(+)	Pseudomonas putida KT2440	3	-- C CAGCAC - CAA CCAC TGCTGC A G GTT GGTG ACGACG C AT T TCAC-- A	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACCGCT GCTGCTG	phoY2	NC_000962 from 913556 to 914197	(-)	Mycobacterium tuberculosis H37Rv	3	-- - ---- CAA CCGC TGCTGCTG GTT GGTG ACGACGAC AT T TCAC	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACCGCT GCTGCTG	phoY2	NC_002945 from 914388 to 915029	(-)	Mycobacterium bovis subsp bovis AF2122/97	3	-- - ---- CAA CCGC TGCTGCTG GTT GGTG ACGACGAC AT T TCAC	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACCGGT GCTGCG	dadX	NC_004431 from 1476306 to 1477376	(+)	Escherichia coli CFT073	3	-- - G---- - CAA CCG TGCTGC G GTT GGT ACGACG C AT T GTCAC A	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACCGTC GGTGATGC TCTG	fhaL	NC_002929 from 3085865 to 3098455	(+)	Bordetella pertussis	3	-- - C GTGA - CAA CCGT G TGCT A CTG GTT GGTG C ACGA GAC AT T T AC-- C	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACCTGC GCTG	speD	NC_003197 from 194201 to 194995	(-)	Salmonella typhimurium LT2	3	-- - ------ - CAA CC TGC GCTG GTT GG ACG CGAC AT T TGTCAC A	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACCTGC GCTG	speD	NC_003198 from 196389 to 197183	(-)	Salmonella enterica enterica serovar Typhi	3	-- - ------ - CAA CC TGC GCTG GTT GG ACG CGAC AT T TGTCAC A	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACCTGC GCTG	speD	NC_004631 from 196380 to 197174	(-)	Salmonella enterica enterica serovar Typhi Ty2	3	-- - ------ - CAA CC TGC GCTG GTT GG ACG CGAC AT T TGTCAC A	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAACGCCA AGCTGCTG	flhB	NC_002929 from 1441767 to 1442921	(+)	Bordetella pertussis	3	-- CG -----A CAA CCA GCTGCTG GTT GGT CGACGAC AT T- GTCACA	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAAGCCAA TCTGCTG	sseB	NC_004431 from 2922456 to 2923241	(-)	Escherichia coli CFT073	3	-- A---- - CAAGCCA T CTGCTG GTTTGGT A GACGAC AT GTCAC C	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAAGCCCG CTTGCTGT G	aer-2	NC_002947 from 2406996 to 2408561	(-)	Pseudomonas putida KT2440	3	-- CGCT-- - CAAGCC TGCTG TG GTTTGG ACGAC AC AT TGTCAC G	A

GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAAGCCTG CGCTG	lppI	NC_000962 from 2291267 to 2291923 (+)	Mycobacterium tuberculosis H37Rv	3	-- CAAGCC GTTTGG AT	------ TGC GCTG ACG CGAC TGTCAC - A A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAAGCCTG CGCTG	lppI	NC_002945 from 2275182 to 2275838 (+)	Mycobacterium bovis subsp bovis AF2122/97	3	-- CAAGCC GTTTGG AT	------ TGC GCTG ACG CGAC TGTCAC - A A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAAGCTGC TGCTG	risA	NC_002929 from 3765257 to 3765991 (-)	Bordetella pertussis	3	-- GTGTCAC	------- TGCTGCTG ACGACGAC AT CAAGC GTTTG AT A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAAGGACC ATGCGCTG	accC	NC_002929 from 9264077 to 9277737 (+)	Bordetella pertussis	3	-- GCTG CAA GTC ACA	GG ----- ACCA TGC GTT TGGT ACG CGAC AT -- GTCAC A A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAAGGCAA AGGTCTGC TG	rpsT	NC_002947 from 7070686 to 7073446 (-)	Pseudomonas putida KT2440	3	-- CA GT G	G A G- - CAAG AG T CTGCTG GTTT TC A GACGAC AT G G AC C A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATAACA ATGCAGCT G	fmtB(mrp)	NC_002745 from 2218145 to 2225590 (-)	Staphylococcus aureus su bsp. aureus N315	3	-- AT	T A A---- A CAA A CA TGC GCTG GTT T GT ACG CGAC - G GTCAC A A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATAACA ATGCAGCT G	fmtB(mrp)	NC_002758 from 2287935 to 2295380 (-)	Staphylococcus aureus su bsp. aureus Mu50	3	-- AT	T A A---- A CAA A CA TGC GCTG GTT T GT ACG CGAC - G GTCAC A A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATAACA ATGCAGCT G	truncated fmtB	NC_003923 from 2238083 to 2240143 (-)	Staphylococcus aureus su bsp. aureus MW2	3	-- AT	T A A---- A CAA A CA TGC GCTG GTT T GT ACG CGAC - G GTCAC A A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATAGCG CCTGCTGC TG	nupC	NC_004337 from 2515842 to 2517083 (+)	Shigella flexneri 2a str. 301	3	-- A T TGG	T-- GC CC CAA G TGCTGCTG GTT C ACGACGAC AT GT AC A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATAGCG CCTGCTGC TG	nupC	NC_004431 from 2795390 to 2796631 (+)	Escherichia coli CFT073	3	-- A T TGG	T-- GC CC CAA G TGCTGCTG GTT C ACGACGAC AT GT AC A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATAGCG CCTGCTGC TG	nupC	NC_004741 from 2494019 to 2495221 (+)	Shigella flexneri 2a str. 2457T	3	-- A T TGG	T-- GC CC CAA G TGCTGCTG GTT C ACGACGAC AT GT AC A

GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATATAG AAGCTGCT GCTA	def	NC_000922 from 1221735 to 1222295 (+)	Chlamydophila pneumoniae CWL029	3	-- TA G AGC A CAA TA A TGCTGCT GTT GT T ACGACGA AT TG G CAC C	A	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATATAG AAGCTGCT GCTA	def	NC_002491 from 1218069 to 1218629 (+)	Chlamydophila pneumoniae J138	3	-- TA G AGC A CAA TA A TGCTGCT GTT GT T ACGACGA AT TG G CAC C	A	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATCACC GGGCCGAT GCGGCTG	glcC	NC_004431 from 3542871 to 3543695 (+)	Escherichia coli CFT073	3	-- T - C G CCGA G CAA C AC G G TGC A GCTG GTT G TG C C ACG CGAC AT T G T A ---- A		
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATCAGG GATACTGC TG	pta	NC_002947 from 891625 to 893712 (-)	Pseudomonas putida KT244 0	3	-- T - G A- A CAA C A GG T CTGCTG GTT G T TC A GACGAC AT T G G AC C	A	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATCCCC GCTTCCTG CTG	tcfA	NC_002929 from 1264436 to 1266379 (+)	Bordetella pertussis	3	-- T C C - C CAA CC CG T T CTGCTG GTT GG GT A A GACGAC AT T T C C C	A	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATCCCG GCCATTTG CTCTG	ruvB	NC_003143 from 2336449 to 2337453 (+)	Yersinia pestis	3	-- T CG CCATT - CAA CC G TGCT A CTG GTT GG T ACGA GAC AT T TG CAC-- C		
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATCCCG GCCATTTG CTCTG	ruvB	NC_004088 from 2482031 to 2483035 (-)	Yersinia pestis KIM	3	-- T CG CCATT - CAA CC G TGCT A CTG GTT GG T ACGA GAC AT T TG CAC-- C		
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATCGCA GCACTGGT GCTG	nupC	NC_004337 from 2515842 to 2517083 (+)	Shigella flexneri 2a str. 301	3	-- T G GCAC- G CAA C CA TG TGCTG GTT G GT AC ACGAC AT T - GTCAC G	A	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAATCTCA CTTTCTGC GCTG	rpsT	NC_002947 from 707068 to 707346 (-)	Pseudomonas putida KT244 0	3	-- T T TT C - CAA C CAC T TGC GCTG GTT G GTG A ACG CGAC AT T - TC C A	A	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CACACAGG TCATCCTT GCGCTG	prcA	NC_002677 from 1576553 to 1577350 (+)	Mycobacterium leprae	3	-- C - G TCATCCT - CA AC A G TGC A GCTG GT TG T T ACG CGAC AT T G G CAC---- A		
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CACATGTT GTACATGC TGCTT	nupC	NC_004337 from 2515842 to 2517083 (+)	Shigella flexneri 2a str. 301	3	-- -- - T TACA T CA C ATG TG A TGCTGCT GT G TGT AC ACGACGA AT TT G C ---- C		
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CACCAATG CTCCTG	lppI	NC_000962 from 2291267 to 2291923 (+)	Mycobacterium tuberculosis H37Rv	3	-- -- A---- C CA CCA TGCT CTG GT GGT ACGA GAC AT TT GTCAC C	A	
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CACCAATG CTCCTG	lppI	NC_002945 from 2275182 to 2275882 (+)	Mycobacterium bovis	3	-- -- A---- C CA CCA TGCT CTG GT GGT ACGA GAC	A	

					38 (+)	subs p bovis AF21 22/97		AT TT GTCAC C				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCACCG CTAACTGC TGCG	ompG	NC_004431 from 1624577 to 1625533 (+)	Escherichia coli CFT073	3	-- -- C CTAAC - CA CCAC G A TGCTGC G GT GGTG C ACGACG C AT TT T AC--- A				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCACCT CCTGCTG	phnV	NC_003198 from 4715 75 to 47236 6 (-)	Salmonella enterica enterica serovar Typhi	3	-- -- C--- C CA A CCAC T CTGCTG GT GGTG A GACGAC AT TT TCAC C				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCACCT CCTGCTG	phnV	NC_004631 from 2508735 to 2509526 (+)	Salmonella enterica enterica serovar Typhi Ty2	3	-- -- C--- C CA A CCAC T CTGCTG GT GGTG A GACGAC AT TT TCAC C				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCACGT AGTGCTTC TG	pilT	NC_002947 from 5816934 to 5817944 (-)	Pseudomonas putida KT244 0	3	-- -- TA T A CA CCACG GTGCT CTG GT GGTGT CACGA GAC AT TT CA C				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCAGCG CCTGCGCT G	oxyR	NC_003197 from 4343080 to 4343997 (+)	Salmonella typhimurium LT2	3	-- -- GC CC - CA A CCA G TGC GCTG GT GGT C ACG CGAC AT TT GT AC A				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCAGCG CCTGCGCT G	oxyR	NC_003198 from 3607204 to 3608121 (-)	Salmonella enterica enterica serovar Typhi	3	-- -- GC CC - CA A CCA G TGC GCTG GT GGT C ACG CGAC AT TT GT AC A				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCAGCG CCTGCGCT G	oxyR	NC_004631 from 3592864 to 3593781 (-)	Salmonella enterica enterica serovar Typhi Ty2	3	-- -- GC CC - CA A CCA G TGC GCTG GT GGT C ACG CGAC AT TT GT AC A				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCATGC TGCTG	MGAT5	NM_002410	Human	3	-- -- ----- CA A CCA TGCTGCTG GT GGT ACGACGAC AT TT GTCAC				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCATTG CTGCCG	ipaH_5	NC_004741 from 2023205 to 2024848 (+)	Shigella flexneri 2a str. 2457T	3	-- -- ---- C A CA CCAT TGCTGC G GT GGTG ACGACG C AT TT TCAC A				
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CACCATTG CTGCCG	ipaH9.8	NC_004337 from 1422064 to 1423779 (-)	Shigella flexneri 2a str	3	-- -- ---- C A CA CCAT TGCTGC G GT GGTG ACGACG C AT TT TCAC A				

						. 301			
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCATTGCTGCCG	sitD	NC_004337 from 1405360 to 1406217 (-)	Shigella flexneri 2a str. 301	3	-- -- ---- C CA CCAT TGCTGC G GT GGTG ACGACG C AT TT TCAC A	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCATTGCTGCCG	sitD	NC_004741 from 1904666 to 1905523 (+)	Shigella flexneri 2a str. 2457T	3	-- -- ---- C CA CCAT TGCTGC G GT GGTG ACGACG C AT TT TCAC A	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCATTTCTGCCGCTG	dnaE	NC_002677 from 1423014 to 1426547 (+)	Mycobacterium leprae	3	-- -- TTC- C CA CCAT TGC GCTG GT GGTG ACG CGAC AT TT TCAC A	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCATTTCTGCCGCTG	pcnA	NC_002677 from 3248268 to 3249728 (-)	Mycobacterium leprae	3	-- -- TTC- C CA CCAT TGC GCTG GT GGTG ACG CGAC AT TT TCAC A	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCATTTCTGCCGCTG	polA	NC_002677 from 1648220 to 1650955 (-)	Mycobacterium leprae	3	-- -- TTC- C CA CCAT TGC GCTG GT GGTG ACG CGAC AT TT TCAC A	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCATTTCTGCCGCTG	truA	NC_002677 from 2343329 to 2344078 (-)	Mycobacterium leprae	3	-- -- TTC- C CA CCAT TGC GCTG GT GGTG ACG CGAC AT TT TCAC A	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCCAGCGTTTGCTGCTT	dadX	NC_004431 from 1476306 to 1477376 (+)	Escherichia coli CFT073	3	-- C- GC T T CA CCA GT TGCTGCT GT GGT CA ACGACGA AT TT GT C C	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCCAGGTGTCGCTGCTG	nicT	NC_000962 from 3166681 to 3167799 (+)	Mycobacterium tuberculosis H37Rv	3	-- C- G TGTC CA CCA G GCTGCTG GT GGT T CGACGAC AT TT G CACA	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCCAGGTGTCGCTGCTG	nicT	NC_002945 from 3123200 to 3124318 (+)	Mycobacterium bovis subsp bovis AF2122/97	3	-- C- G TGTC CA CCA G GCTGCTG GT GGT T CGACGAC AT TT G CACA	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACCTTTCTGCTGCTC	risA	NC_002929 from 3765257 to 3765991 (-)	Bordetella pertussis	3	-- -- T TC-- C CA CC T TGCTGCT GT GG G ACGACGA AT TT T TCAC C	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACGCCATATGTGTTTGTGCTG	ipaH_5	NC_004741 from 2023205 to 2024848 (+)	Shigella flexneri 2a str. 2457T	3	-- C TGTGTT - CA GCCATA TG TGCTG GT TGGTGT AC ACGAC AT T CAC--- G	A
GAM353678	Human	CAGCAGCACACTGTGGTTTGTA	CACGCCATATGTGTTTGTGCTG	ipaH9.8	NC_004337 from 1422064 to 1423779 (-)	Shigella flexneri 2a str. 301	3	-- C TGTGTT - CA GCCATA TG TGCTG GT TGGTGT AC ACGAC AT T CAC--- G	A
GAM353678	Human	CAGCAGCACACTGTGG	CACGCCATATGTGTTT	sitD	NC_004337 from 14053	Shigella fle	3	-- C TGTGTT - CA GCCATA TG	A

		TTTGTA	GTGCTG		60 to 14062 17 (-)	xneri 2a str . 301		TGCTG GT TGGTGT AC ACGAC AT T CAC--- G	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CACGCCAT ATGTGTTT GTGCTG	sit D	NC_004741 from 1904666 to 1905523 (+)	Shigella flexneri 2a str. 2457T	3	-- C TGTGTT - CA GCCATA TG A TGCTG GT TGGTGT AC ACGAC AT T CAC--- G	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGAACAC TGTTACCG CTGCTG	rbs R	NC_004337 from 3947708 to 3948700 (+)	Shigella flexneri 2a str. 301	3	-- A T TACC CAGA CAC GT A GCTGCTG GTTT GTG CA CGACGAC AT G T C--A	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGAACAC TGTTACCG CTGCTG	rbs R	NC_004431 from 4439260 to 4440252 (+)	Escherichia coli CFT073	3	-- A T TACC CAGA CAC GT A GCTGCTG GTTT GTG CA CGACGAC AT G T C--A	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGAACAC TGTTACCG CTGCTG	rbs R	NC_004741 from 3824594 to 3825577 (-)	Shigella flexneri 2a str. 2457T	3	-- A T TACC CAGA CAC GT A GCTGCTG GTTT GTG CA CGACGAC AT G T C--A	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGAAGCA TGAACATT GCTGCTG	rbs R	NC_004337 from 3947708 to 3948700 (+)	Shigella flexneri 2a str. 301	3	-- G G AACAT CA AA CATG TGCTGCTG A GT TT GTGT ACGACGAC AT - G CAC--	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGAAGCA TGAACATT GCTGCTG	rbs R	NC_004741 from 3824594 to 3825577 (-)	Shigella flexneri 2a str. 2457T	3	-- G G AACAT CA AA CATG TGCTGCTG A GT TT GTGT ACGACGAC AT - G CAC--	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGACGAT CTCCTGCT G C	fep	NC_002516 from 4653508 to 4654305 (-)	Pseudomonas aeruginosa PA01	3	-- G C--- C A CAGAC AT T CTGCTG GTTTG TG A GACGAC AT G TCAC C	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGACTCA GCTGCTGC TC	pilT	NC_002947 from 5816934 to 5817944 (-)	Pseudomonas putida KT2440	3	-- T GC--- C A CAGAC CA TGCTGCT GTTTG GT ACGACGA AT - GTCAC C	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGCAGGC TTTGCTGC TG	cII	NC_003198 from 4537312 to 4537533 (+)	Salmonella enterica enterica serovar Typhi	3	-- - - G C T CAG C A A G T TGCTGCTG GTT G T T T A ACGACGAC AT T G G C C	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CAGCAGGC TTTGCTGC TG	cII	NC_004631 from 4520121 to 4520342 (+)	Salmonella enterica enterica serovar Typhi Ty2	3	-- - - G C T CAG C A A G T TGCTGCTG GTT G T T T A ACGACGAC AT T G G C C	
GAM3 3678	Hum an	CAGCAGCA CACTGTGG	CAGCCACA GCTGCTG	gad	NC_002947 from 4871648	Pseudomonas	3	-- - ----A CAG A CCAC GCTGCTG GTT	

		TTTGTA			25 to 48729 29 (+)	putida KT244 0		GGTG TCACA	CGACGAC AT	T
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAGCCAGG TTTTGCTC TG	phnV	NC_003198 from 4715 75 to 47236 6 (-)	Salmonella enterica enterica serovar Typhi	3	-- CAG CCA G T TGCT CTG GTT GGT T A ACGA GAC AT T G C C	- C	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAGCCAGG TTTTGCTC TG	phnV	NC_004631 from 25087 35 to 25095 26 (+)	Salmonella enterica enterica serovar Typhi Ty2	3	-- CAG CCA G T TGCT CTG GTT GGT T A ACGA GAC AT T G C C	- C	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAGCGAGG CCTCGTGC TGCTG	tcfA	NC_002929 from 12644 36 to 12663 79 (+)	Bordetella pertussis	3	-- C A G GTT G T T ACGACGAC AT CAC--	- G G CCTCG TGCTGCTG T G G	CAG A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAGCGCTT GGTGATGC TGCTG	uhpA	NC_003143 from 45227 90 to 45233 80 (-)	Yersinia pestis	3	-- C TGGTG TGCTGCTG G GTCAC ACGACGAC AT TG T	CG T A -	CAG GTT A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CAGGCGCA GGGTGTGC TGCTG	cysQ	NC_002947 from 3151 84 to 31598 4 (+)	Pseudomonas putida KT244 0	3	-- GGTGTGCTGCTG TCACACGACGAC AT G	G G CAGGC CA GTTTG GT -	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CATACCTC CCGCACTG CTGCCG	pbpG	NC_002947 from 43237 07 to 43246 33 (+)	Pseudomonas putida KT244 0	3	-- CA ACC C G GT TGG G TCAC--	T T CCGCAC TGCTGC ACGACG C AT T A	C A T
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CATATCTG CTGCTG	ung	NC_000907 from 186 76 to 19335 (+)	Haemophilus influenzae R d	3	-- TGTCAC	T ------ CA ATC TGCTGCTG GT TGG ACGACGAC AT T	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CATCCACA CGCTGCTG	ssb	NC_002947 from 5710 27 to 57157 2 (+)	Pseudomonas putida KT244 0	3	-- CCACA GGTGT TT	T- GCTGCTG CGACGAC AT CACA	---C CA GT	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CATCCATA TCGCCATT GCTGGTG	rbsR	NC_004431 from 44392 60 to 44402 52 (+)	Escherichia coli CFT073	3	-- C TGCTG TG C CA	T- G ACGAC AC AT CA ----	TC CCAT CA TGT TT G A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CATCGCGG GCGCGCTG CTGCTC	glpC	NC_003143 from 42896 50 to 42908 97 (-)	Yersinia pestis	3	-- TGCTGCT ACGACGA AT CAC--	TCG G CGCGC C CA CG G GT GT T TTG G C	A
GAM3536 78	Human	CAGCAGCA CACTGTGG TTTGTA	CATCGCGG GCGCGCTG CTGCTC	glpC	NC_004088 from 4546 77 to 45604 7 (+)	Yersinia pestis KIM	3	-- TGCTGCT ACGACGA AT CAC--	TCG G CGCGC C CA CG G GT GT T TTG G C	A
GAM3536 78	Human	CAGCAGCA	CATGTCGG	dna	NC_002677 f	Mycobac	3	--	T GT GTGGA	A

3678	an	CACTGTGG TTTGTA	TGGTGGAT GCTGCTT	E	rom 14 to 47	14230 14265 (+)	teriu m leprae	3	T CA GTCG G TGCTGCT GT TGGT C ACGACGA AT T GT AC--- C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CATGTCGG TGGTGGAT GCTGCTT	pcn A	NC_002677 rom 68 to 28	f 32482 32497 (-)	Mycobac teriu m leprae	3	-- T GT GTGGA T CA GTCG G A TGCTGCT GT TGGT C ACGACGA AT T GT AC--- C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CATGTCGG TGGTGGGT GCTGCTT	pol A	NC_002677 rom 20 to 55	f 16482 16509 (-)	Mycobac teriu m leprae	3	-- T GT GTGGG T CA GTCG G A TGCTGCT GT TGGT C ACGACGA AT T GT AC--- C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CATGTCGG TGGTGGGT GCTGCTT	tru A	NC_002677 rom 29 to 78	f 23433 23440 (-)	Mycobac teriu m leprae	3	-- T GT GTGGG T CA GTCG G A TGCTGCT GT TGGT C ACGACGA AT T GT AC--- C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CCCGTGCT GCTT	omp G	NC_004431 rom 77 to 33	f 16245 16255 (+)	Escheri chia coli CFT073	3	-- --- ----- T A C CCG TGCTGCT G GGT ACGACGA AT TTT GTCAC C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CCCTCGGT GCTGCTG	flh B	NC_002929 rom 67 to 21	f 14417 14429 (+)	Bordete lla p ertussi s	3	-- --- T -- C CC A CGG TGCTGCTG G GG GTC ACGACGAC AT TTT T AC	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CGAACCAC CGATGCTG TG	aer -2	NC_002947 rom 96 to 61	f 24069 24085 (-)	Pseudom onas putida KT244 0	3	-- C A- - A CGAACCAC G TGCTG TG GTTTGGTG C ACGAC AC AT T AC G	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CGAACGTG CTGCTG	prc A	NC_002677 rom 53 to 50	f 15765 15773 (+)	Mycobac teriu m leprae	3	-- G------ CGAAC A TGCTGCTG GTTTG ACGACGAC AT GTGTCAC	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CGACCACC GCGTGGTG CTG	van B	NC_002516 rom 20 to 73	f 55041 55050 (+)	Pseudom onas aerugin osa P A01	3	-- - C C G CGA A CCAC G GTG TGCTG GTT GGTG C CAC ACGAC AT T T A G	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CGACTGCT GCTG	pch A	NC_002516 rom 20 to 50	f 47451 47465 (+)	Pseudom onas aerugin osa P A01	3	-- - ------- CGA C A TGCTGCTG GTT G ACGACGAC AT T GTGTCAC	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CGAGCGAT GCTGCTT	dsd A	NC_003197 rom 53 to 75	f 40044 40057 (+)	Salmone lla t yphimur ium L T2	3	-- G ----- T A CGAGC A TGCTGCT GTTTG T ACGACGA AT G GTCAC C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CGAGGGAT GTAGTGCT GCTC	nic T	NC_000962 rom 81 to 99	f 31666 31677 (+)	Mycobac teriu m tubercu los is H37Rv	3	-- GG TA C A CGAG ATG GTGCTGCT GTTT TGT CACGACGA AT GG CA C	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CGAGGGAT GTAGTGCT GCTC	nic T	NC_002945 rom 00 to 18	f 31232 31243 (+)	Mycobac teriu m bovis subs p bovis AF21	3	-- GG TA C A CGAG ATG GTGCTGCT GTTT TGT CACGACGA AT GG CA C	

22/97

GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGCCAGAT TGCTGCTG	yabO	NC_004431 from 61489 to 62148 (-)	Escherichia coli CFT073	3	-- -- G T-- CG CCA A TGCTGCTG GT GGT T ACGACGAC AT TT G CAC	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGCCGGTT GCTGCTG	pchA	NC_002516 from 47451 20 to 47465 50 (+)	Pseudomonas aeruginosa PA01	3	-- -- GT--- CG CCG TGCTGCTG GT GGT ACGACGAC AT TT GTCAC	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGCCGGTT GCTGCTT	fepC	NC_002516 from 46535 08 to 46543 05 (-)	Pseudomonas aeruginosa PA01	3	-- -- GT--- T CG CCG TGCTGCT GT GGT ACGACGA AT TT GTCAC C	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGCTGCTG CTG	livH	NC_002929 from 11447 29 to 11456 07 (+)	Bordetella pertussis	3	-- -- ------- CG C TGCTGCTG GT G ACGACGAC AT TT GTGTCAC	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGGAATTT GCTGCTG	yciE	NC_004431 from 15586 41 to 15591 47 (-)	Escherichia coli CFT073	3	-- -- T--- CGGA AT TGCTGCTG GTTT TG ACGACGAC AT GG TCAC	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGTCCACG CGGGTGGT GCTGCTC	flhB	NC_002929 from 14417 67 to 14429 21 (+)	Bordetella pertussis	3	-- T- CG GTGG C CG CCACG G TGCTGCT GT GGTGT C ACGACGA AT TT CA ---- C	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGTCCATC TTGCTGCT C	pbpG	NC_002947 from 43237 07 to 43246 33 (+)	Pseudomonas putida KT244 0	3	-- T- CT-- C CG CCAT TGCTGCT GT GGTG ACGACGA AT TT TCAC C	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGTCCTGC TGCTG	acoR	NC_002516 from 46395 01 to 46413 78 (-)	Pseudomonas aeruginosa PA01	3	-- T- ------ CG CC TGCTGCTG GT GG ACGACGAC AT TT TGTCAC	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CGTGCCTG CTGCTC	aceK	NC_002947 from 51847 42 to 51864 57 (-)	Pseudomonas putida KT244 0	3	-- T ------ C CG GCC TGCTGCT GT TGG ACGACGA AT T TGTCAC C	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CTAAAGTG CTGCTG	recG	NC_002677 from 20147 23 to 20169 54 (-)	Mycobacterium leprae	3	-- T -- G---- C AA A TGCTGCTG G TT T ACGACGAC AT T GG GTCAC	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CTAACACG CGCTGCTC TG	ung	NC_000907 from 18676 to 19335 (+)	Haemophilus influenzae R d	3	-- T - CGC - C AAC ACG TGCT CTG G TTG TGT ACGA GAC AT T G CAC C	A			
GAM35 3678	Human	CAGCAGCA CACTGTGG TTTGTA	CTAACCTG TATCTGCT G	cII	NC_003198 from 45373 12 to 45375 33 (+)	Salmonella enterica enterica serovar Typhi	3	-- T TGTA-- - C AACC T CTGCTG G TTGG A GACGAC AT T TGTCAC C	A			
GAM35 3678	Human	CAGCAGCA	CTAACCTG	cII	NC_004631 f	Salmone	3	-- T TGTA-- - C	A			

3678	an	CACTGTGG TTTGTA	TATCTGCT G		rom 21 to 42	45201 45203 (+)	lla e nterica ente rica serovar Typhi Ty2	AACC TTGG	T CTGCTG A GACGAC TGTCAC	G AT T C
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTACCTGC CTGCTGCT	uhp G A	NC_003143 rom 90 to 80	f 45227 45233 (-)	Yersini a pes tis	3 -- T - TGCC-- TGCTGCTG ACGACGAC TGTCAC	C A CC G T GG AT T T	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTAGCCCT GCTGCTC	aco R	NC_002516 rom 01 to 78	f 46395 46413 (-)	Pseudom onas aerugin osa P A01	3 -- T C AGCC G TTGG AT T TGTCAC	C----- TGCTGCT ACGACGA C	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTCCTGCT GCTG	ssb	NC_002947 rom 27 to 2	f 5710 57157 (+)	Pseudom onas putida KT244 0	3 -- T-- TGCTGCTG ACGACGAC TGTCAC	------ C CC G GG AT TTT	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTCGGGTT TCTTGCTG CTG	fha L	NC_002929 rom 65 to 55	f 30858 30984 (+)	Bordete lla p ertussi s	3 -- T-- G GTT CT G T A G GTC C-	C C T TGCTGCTG G G ACGACGAC AT TTT	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTGACCTT GCTGCTC	pta	NC_002947 rom 25 to 2	f 8916 89371 (-)	Pseudom onas putida KT244 0	3 -- T C GACC G TTGG AT T TGTCAC	T----- TGCTGCT ACGACGA C	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTGCCTGC TGCTC	orn	NC_003143 rom 31 to 6	f 3783 37887 (+)	Yersini a pes tis	3 -- T - C G CC G T GG AT T T	------ TGCTGCT ACGACGA TGTCAC C	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTGCGTGC TGCTT	glp D	NC_004310 rom 63 to 4	f 2107 21227 (+)	Brucell a sui s 1330	3 -- T - G C G T G AT T T GTGTCAC	------ TGCTGCT ACGACGA C	T A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTTACTTG CTGCTC	sse B	NC_004431 rom 56 to 41	f 29224 29232 (-)	Escheri chia coli CFT073	3 -- TT C ACT G TGG AT TT TGTCAC	------ TGCTGCT ACGACGA C	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTTCCTGC TGCTT	def	NC_000922 rom 35 to 95	f 12217 12222 (+)	Chlamyd ophil a pneumon iae CWL029	3 -- TT- C G AT TTT	------ CC GG TGTCAC	T A C
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	CTTCCTGC TGCTT	def	NC_002491 rom 69 to 29	f 12180 12186 (+)	Chlamyd ophil a pneumon iae J138	3 -- TT- C G AT TTT	------ CC GG TGTCAC	T A C

Replace paragraph 0159 with the following paragraph.

It is appreciated that the specific functions and accordingly the utilities of each of a plurality of GAM oligonucleotides that are described by Fig. 1 are correlated with and may be deduced from the

identity of the GAM TARGET GENES inhibited thereby, and whose functions are set forth in Table 8, hereby incorporated herein. Table 8 , lines 685695-687709 shows data relating to the function and utilities of GAM RNA as set forth in SEQ ID NO: 348.

After paragraph 0159, add the following Table 8.

Table 8

GAM NAME	GAM RNA SEQUENCE	GAM ORGANISM	TARGET	TARGET ORGANISM	GAM FUNCTION	GAM POS
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	accC	Bordetella pertussis	GAM353678 is a human miRNA-like oligonucleotide, which targets biotin carboxylase (accC, NC_002929 from 926407 to 927777 (+)), a bacterial target gene encoded by the Bordetella per tussis genome, as part of an anti-bacterial host defense mecha nism. accC BINDING SITE 1 and accC BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the accC gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1.The nucleotide sequences of accC BINDING SITE 1 and accC BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. A function of GAM353678 is to inhibit accC, a GAM353678 bacter ial target gene which is associated with Bordetella pertussis infection, as part of an anti-bacterial host defense mechanism . Accordingly, the utilities of GAM353678 include the diagnosi s, prevention and treatment of Bordetella pertussis infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	aceK	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets isocitrate dehydrogenase kinase/phosphatase (aceK, NC_002947 from 5184742 to 5186457 (-)), a bacterial target gene enco ded by the Pseudomonas putida KT2440 genome, as part of an ant i-bacterial host defense mechanism. aceK BINDING SITE 1 and aceK BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the aceK gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of aceK BINDING SITE 1 and aceK BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aceK, a GAM353678 bacterial target gene which is associated with Pseudomonas put ida KT2440 infection, as part of an anti-bacterial host defens e mechanism. Accordingly, the utilities of	A

					GAM353678 include t he diagnosis, prevention and treatment of Pseudomonas putida K T2440 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	acoR	Pseudomonas aerugi nosa PA01	GAM353678 is a human miRNA-like oligonucleotide, which targets transcriptional regulator AcoR (acoR, NC_002516 from 463950 1 to 4641378 (-)), a bacterial target gene encoded by the Ps eudomonas aeruginosa PA01 genome, as part of an anti-bacterial host defense mechanism. acoR BINDING SITE 1 and acoR BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the acoR gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of acoR BINDING SITE 1 and acoR BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit acoR, a GAM353678 bacterial target gene which is associated with Pseudomonas aer uginosa PA01 infection, as part of an anti-bacterial host defe nse mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas aerugi nosa PA01 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	aer-2	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets aerotaxis receptor Aer-2 (aer-2, NC_002947 from 2406996 to 2408561 (-)), a bacterial target gene encoded by the Pseudom onas putida KT2440 genome, as part of an anti-bacterial host d efense mechanism. aer-2 BINDING SITE 1 and aer-2 BINDING SITE 2 are bacterial ta rget binding sites that are found in the untranslated regions of mRNA encoded by the aer-2 gene, corresponding to target bin ding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of aer-2 BINDING SITE 1 and aer-2 BINDING SITE 2, and the complementary seconda ry structure to the nucleotide sequence of GAM353678 RNA are s et forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aer-2, a GAM353678 bacterial target gene which is associated with Pseudomonas pu tida KT2440 infection, as part of an anti-bacterial host defen se mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida KT2440 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	amtB	Shigella flexneri 2a str. 301	GAM353678 is a human miRNA-like oligonucleotide, which targets probable ammonium transporter (amtB, NC_004337 from 408059 to 409345 (+)), a bacterial target gene encoded by the Shi gella flexneri 2a str. 301 genome, as part of an anti-bacteria l host defense mechanism. amtB BINDING SITE 1 and amtB BINDING SITE	A

					2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the amtB gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of amtB BINDING SITE 1 and amtB BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit amtB, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 301 infection, as part of an anti-bacterial host de fense mechanism. Accordingly, the utilities of GAM353678 inclu de the diagnosis, prevention and treatment of Shigella flexner i 2a str. 301 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	amtB	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Probable ammonium transporter (amtB, NC_004431 from 547616 to 548902 (+)), a bacterial target gene encoded by the Esc herichia coli CFT073 genome, as part of an anti-bacterial host defense mechanism. amtB BINDING SITE 1 and amtB BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the amtB gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of amtB BINDING SITE 1 and amtB BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit amtB, a GAM353678 bacterial target gene which is associated with Escherichia col i CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	amtB	Shigella flexneri 2a str. 2457T	GAM353678 is a human miRNA-like oligonucleotide, which targets probable ammonium transporter (amtB, NC_004741 from 407860 to 409146 (+)), a bacterial target gene encoded by the Shi gella flexneri 2a str. 2457T genome, as part of an anti-bacter ial host defense mechanism. amtB BINDING SITE 1 and amtB BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the amtB gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of amtB BINDING SITE 1 and amtB BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit amtB, a GAM353678	A

					bacterial target gene which is associated with Shigella flexne ri 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 inc lude the diagnosis, prevention and treatment of Shigella flexn eri 2a str. 2457T infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	aroA	Neisseria meningitidis Z2491	GAM353678 is a human miRNA-like oligonucleotide, which targets 5-enolpyruvoylshikimate-3-phosphate synthase (aroA, NC_003116 from 1557502 to 1558803 (+)), a bacterial target gene enc oded by the Neisseria meningitidis Z2491 genome, as part of an anti-bacterial host defense mechanism. aroA BINDING SITE 1 and aroA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the aroA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of aroA BINDING SITE 1 and aroA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aroA, a GAM353678 bacterial target gene which is associated with Neisseria menin gitidis Z2491 infection, as part of an anti-bacterial host def ense mechanism. Accordingly, the utilities of GAM353678 includ e the diagnosis, prevention and treatment of Neisseria meningi tidis Z2491 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	aroD	Leptospira interrogans serovar lai str. 56601	GAM353678 is a human miRNA-like oligonucleotide, which targets 3-dehydroquinate dehydratase (aroD, NC_004342 from 48128 to 48832 (-)), a bacterial target gene encoded by the Lept ospira interrogans serovar lai str. 56601 genome, as part of a n anti-bacterial host defense mechanism. aroD BINDING SITE 1 and aroD BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the aroD gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of aroD BINDING SITE 1 and aroD BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aroD, a GAM353678 bacterial target gene which is associated with Leptospira inte rrogans serovar lai str. 56601 infection, as part of an anti-b acterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Leptospira interrogans serovar lai str. 56601 infection and as sociated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	aroH	Shigella flexneri 2a str. 3	GAM353678 is a human miRNA-like oligonucleotide, which targets 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	A

				01	(DAHP syn thetase, tryptophan repressible) (aroH, NC_004337 from 15575 27 to 1558573 (-)), a bacterial target gene encoded by the S higella flexneri 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. aroH BINDING SITE 1 and aroH BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the aroH gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of aroH BINDING SITE 1 and aroH BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aroH, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 301 infection, as part of an anti-bacterial host de fense mechanism. Accordingly, the utilities of GAM353678 inclu de the diagnosis, prevention and treatment of Shigella flexner i 2a str. 301 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	avtA	Shigella flexneri 2a str. 301	GAM353678 is a human miRNA-like oligonucleotide, which targets alanine-alpha-ketoisovalerate (or valine-pyruvate) transamina se, transaminase C (avtA, NC_004337 from 3721175 to 3722533 (+)), a bacterial target gene encoded by the Shigella flexne ri 2a str. 301 genome, as part of an anti-bacterial host defen se mechanism. avtA BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region of mRNA encoded by th e avtA gene, corresponding to a target binding site such as BI NDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. T he nucleotide sequences of avtA BINDING SITE, and the compleme ntary secondary structure to the nucleotide sequence of GAM353 678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit avtA, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 301 infection, as part of an anti-bacterial host de fense mechanism. Accordingly, the utilities of GAM353678 inclu de the diagnosis, prevention and treatment of Shigella flexner i 2a str. 301 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	avtA	Shigella flexneri 2a str. 2457T	GAM353678 is a human miRNA-like oligonucleotide, which targets alanine-alpha-ketoisovalerate/valine-pyruvate transaminase C (avtA, NC_004741 from 4052685 to 4053938 (-)), a bacterial target gene encoded by the Shigella flexneri 2a str. 2457T ge nome, as part of an anti-bacterial host defense mechanism. avtA BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region of mRNA encoded by th e avtA gene, corresponding to a target binding site such as BI NDING SITE I, BINDING SITE II or BINDING SITE III of	A

					Fig. 1. T he nucleotide sequences of avtA BINDING SITE, and the compleme ntary secondary structure to the nucleotide sequence of GAM353 678 RNA are set forth in Tables 6-7, hereby incorporated herei n. Another function of GAM353678 is to inhibit avtA, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 inc lude the diagnosis, prevention and treatment of Shigella flexn eri 2a str. 2457T infection and associated clinical conditions	
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	cII	Salmonell a enteric a enteric a serovar Typhi Ty 2	GAM353678 is a human miRNA-like oligonucleotide, which targets transcriptional regulatory protein (cII, NC_004631 from 452 0121 to 4520342 (+)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi Ty2 genome, as par t of an anti-bacterial host defense mechanism. cII BINDING SITE 1 and cII BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of m RNA encoded by the cII gene, corresponding to target binding s ites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of cII BINDING SITE 1 a nd cII BINDING SITE 2, and the complementary secondary structu re to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit cII, a GAM353678 b acterial target gene which is associated with Salmonella enterica enterica serovar Typhi Ty2 infection, as part of an anti-b acterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella enterica enterica serovar Typhi Ty2 infection and a ssociated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	cII	Salmonell a enteric a enteric a serovar Typhi	GAM353678 is a human miRNA-like oligonucleotide, which targets transcriptional regulatory protein (cII, NC_003198 from 453 7312 to 4537533 (+)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi genome, as part of an anti-bacterial host defense mechanism. cII BINDING SITE 1 and cII BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of m RNA encoded by the cII gene, corresponding to target binding s ites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of cII BINDING SITE 1 a nd cII BINDING SITE 2, and the complementary secondary structu re to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit cII, a GAM353678 b acterial target gene which is associated with Salmonella enter ica enterica serovar Typhi infection, as part of an anti-bacte rial host defense mechanism. Accordingly,	A

					the utilities of GAM 353678 include the diagnosis, prevention and treatment of Salm onella enterica enterica serovar Typhi infection and associate d clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	cysM	Salmonella typhimurium LT2	GAM353678 is a human miRNA-like oligonucleotide, which targets cysteine synthase B (cysM, NC_003197 from 2551651 to 255256 2 (-)), a bacterial target gene encoded by the Salmonella ty phimurium LT2 genome, as part of an anti-bacterial host defens e mechanism. cysM BINDING SITE 1 and cysM BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the cysM gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of cysM BINDING SITE 1 and cysM BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit cysM, a GAM353678 bacterial target gene which is associated with Salmonella typh imurium LT2 infection, as part of an anti-bacterial host defen se mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella typhimur ium LT2 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	cysQ	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets 3'(2'),5'-bisphosphate nucleotidase (cysQ, NC_002947 from 315184 to 315984 (+)), a bacterial target gene encoded by t he Pseudomonas putida KT2440 genome, as part of an anti-bacter ial host defense mechanism. cysQ BINDING SITE 1 and cysQ BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the cysQ gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of cysQ BINDING SITE 1 and cysQ BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit cysQ, a GAM353678 bacterial target gene which is associated with Pseudomonas put ida KT2440 infection, as part of an anti-bacterial host defens e mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida K T2440 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	dadX	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Alanine racemase, catabolic (dadX, NC_004431 from 1476306 to 1477376 (+)), a bacterial target gene encoded by the Esche richia coli CFT073 genome, as part of an anti-bacterial host d efense mechanism. dadX BINDING SITE 1 and dadX BINDING SITE 2 are bacterial targ et binding sites that are	A

					found in the untranslated regions of mRNA encoded by the dadX gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of dadX BINDING SITE 1 and dadX BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit dadX, a GAM353678 bacterial target gene which is associated with Escherichia col i CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	def	Chlamydophila pneumoniae CWL029	GAM353678 is a human miRNA-like oligonucleotide, which targets Polypeptide Deformylase (def, NC_000922 from 1221735 to 122 2295 (+)), a bacterial target gene encoded by the Chlamydoph ila pneumoniae CWL029 genome, as part of an anti-bacterial host defense mechanism. def BINDING SITE 1 and def BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the def gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of def BINDING SITE 1 and def BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit def, a GAM353678 b acterial target gene which is associated with Chlamydophila pn eumoniae CWL029 infection, as part of an anti-bacterial host d efense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Chlamydophila p neumoniae CWL029 infection and associated clinical conditions.	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	def	Chlamydophila pneumoniae J138	GAM353678 is a human miRNA-like oligonucleotide, which targets polypeptide deformylase (def, NC_002491 from 1218069 to 121 8629 (+)), a bacterial target gene encoded by the Chlamydoph ila pneumoniae J138 genome,as part of an anti-bacterial host defense mechanism. def BINDING SITE 1 and def BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of m RNA encoded by the def gene, corresponding to target binding s ites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of def BINDING SITE 1 a nd def BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit def, a GAM353678 b acterial target gene which is associated	A

					with Chlamydophila pn eumoniae J138 infection, as part of an anti-bacterial host def ense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Chlamydophila pne umoniae J138 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	dnaE	Mycobacterium leprae	GAM353678 is a human miRNA-like oligonucleotide, which targets DNA polymerase III, [alpha] subunit (dnaE, NC_002677 from 1423014 to 1426547 (+)), a bacterial target gene encoded by the Mycobacterium leprae genome, as part of an anti-bacterial host defense mechanism. dnaE BINDING SITE 1 through dnaE BINDING SITE 3 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the dnaE gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of dnaE BINDING SITE 1 through dnaE BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA ar e set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit dnaE, a GAM353678 bacterial target gene which is associated with Mycobacterium l eprae infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium leprae infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	dsdA	Salmonella typhimurium LT2	GAM353678 is a human miRNA-like oligonucleotide, which targets D-serine deaminase (dsdA, NC_003197 from 4004453 to 4005775 (+)), a bacterial target gene encoded by the Salmonella typ himurium LT2 genome, as part of an anti-bacterial host defense mechanism. dsdA BINDING SITE 1 and dsdA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the dsdA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of dsdA BINDING SITE 1 and dsdA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit dsdA, a GAM353678 bacterial target gene which is associated with Salmonella typh imurium LT2 infection, as part of an anti-bacterial host defen se mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella typhimurium LT2 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	fepC	Pseudomonas aerugi nosa PA01	GAM353678 is a human miRNA-like oligonucleotide, which targets ferric enterobactin transport protein FepC (fepC, NC_002516 f rom 4653508 to 4654305 (-)), a bacterial target gene encoded by the Pseudomonas aeruginosa PA01 genome, as	A

					part of an an ti-bacterial host defense mechanism. fepC BINDING SITE 1 and fepC BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the fepC gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of fepC BINDING SITE 1 and fepC BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit fepC, a GAM353678 bacterial target gene which is associated with Pseudomonas aer uginosa PA01 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas aerugi nosa PA01 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	fhaL	Bordetella pertussis	GAM353678 is a human miRNA-like oligonucleotide, which targets adhesin (fhaL, NC_002929 from 3085865 to 3098455 (+)), a bacterial target gene encoded by the Bordetella pertussis genome, as part of an anti-bacterial host defense mechanism. fhaL BINDING SITE 1 and fhaL BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the fhaL gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of fhaL BINDING SITE 1 and fhaL BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit fhaL, a GAM353678 bacterial target gene which is associated with Bordetella pert ussis infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Bordetella pertussis infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	flhB	Bordetella pertussis	GAM353678 is a human miRNA-like oligonucleotide, which targets flagellar biosynthetic protein FlhB (flhB, NC_002929 from 1 441767 to 1442921 (+)), a bacterial target gene encoded by t he Bordetella pertussis genome, as part of an anti-bacterial h ost defense mechanism. flhB BINDING SITE 1 through flhB BINDING SITE 3 are bacterial target binding sites that are found in the untranslated region s of mRNA encoded by the flhB gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of flhB BINDING SITE 1 through flhB BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby	A

					incorporated herein. Another function of GAM353678 is to inhibit flhB, a GAM353678 bacterial target gene which is associated with Bordetella pert ussis infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Bordetella pertussis infe ction and associated clinical conditions	
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	fmtB(mr p)	Staphyloc occus aur eus subsp . aureus N315	GAM353678 is a human miRNA-like oligonucleotide, which targets FmtB protein (fmtB(mrp), NC_002745 from 2218145 to 2225590 (-)), a bacterial target gene encoded by the Staphylococcus aureus subsp. aureus N315 genome, as part of an anti-bacterial host defense mechanism. fmtB(mrp) BINDING SITE 1 and fmtB(mrp) BINDING SITE 2 are bact erial target binding sites that are found in the untranslated regions of mRNA encoded by the fmtB(mrp) gene, corresponding t o target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of fm tB(mrp) BINDING SITE 1 and fmtB(mrp) BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporate d herein. Another function of GAM353678 is to inhibit fmtB(mrp), a GAM35 3678 bacterial target gene which is associated with Staphyloco ccus aureus subsp. aureus N315 infection, as part of an anti-b acterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Staphylococcus aureus subsp. aureus N315 infection and associated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	fmtB(mr p)	Staphyloc occus aur eus subsp . aureus Mu50	GAM353678 is a human miRNA-like oligonucleotide, which targets FmtB protein (fmtB(mrp), NC_002758 from 2287935 to 2295380 (-)), a bacterial target gene encoded by the Staphylococcus aureus subsp. aureus Mu50 genome, as part of an anti-bacterial host defense mechanism. fmtB(mrp) BINDING SITE 1 and fmtB(mrp) BINDING SITE 2 are bact erial target binding sites that are found in the untranslated regions of mRNA encoded by the fmtB(mrp) gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of fm tB(mrp) BINDING SITE 1 and fmtB(mrp) BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporate d herein. Another function of GAM353678 is to inhibit fmtB(mrp), a GAM35 3678 bacterial target gene which is associated with Staphylococcus aureus subsp. aureus Mu50 infection, as part of an anti-b acterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Staphylococcus aureus subsp.	A

					aureus Mu50 infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	ftsY	Chlamydophila pneumoniae J138	GAM353678 is a human miRNA-like oligonucleotide, which targets cell division protein ftsY (ftsY, NC_002491 from 1113127 to 1113999 (-)), a bacterial target gene encoded by the Chlamy dophila pneumoniae J138 genome, as part of an anti-bacterial host defense mechanism. ftsY BINDING SITE 1 and ftsY BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ftsY gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of ftsY BINDING SITE 1 and ftsY BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ftsY, a GAM353678 bacterial target gene which is associated with Chlamydophila pneumoniae J138 infection, as part of an anti-bacterial host de fense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Chlamydophila pn eumoniae J138 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	ftsY	Chlamydophila pneumoniae CWL029	GAM353678 is a human miRNA-like oligonucleotide, which targets Cell Division Protein FtsY (ftsY, NC_000922 from 1115427 to 1116299 (-)), a bacterial target gene encoded by the Chlamy dophila pneumoniae CWL029 genome, as part of an anti-bacterial host defense mechanism. ftsY BINDING SITE 1 and ftsY BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the ftsY gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of ftsY BINDING SITE 1 and ftsY BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ftsY, a GAM353678 bacterial target gene which is associated with Chlamydophila pneumoniae CWL029 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Chlamydophila pneumoniae CWL029 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	gad	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets guanine aminohydrolase (gad, NC_002947 from 4871625 to 4872 929 (+)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. gad BINDING SITE 1 and gad BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of m RNA	A

					encoded by the gad gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of gad BINDING SITE 1 and gad BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth i n Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit gad, a GAM353678 b acterial target gene which is associated with Pseudomonas puti da KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida KT 2440 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glcC	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Glc operon transcriptional activator (glcC, NC_004431 from 3542871 to 3543695 (+)), a bacterial target gene encoded by the Escherichia coli CFT073 genome, as part of an anti-bacteri al host defense mechanism. glcC BINDING SITE 1 and glcC BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the glcC gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of glcC BINDING SITE 1 and glcC BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glcC, a GAM353678 bacterial target gene which is associated with Escherichia coli CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glgP	Salmonella enterica enterica serovar Typhi Ty2	GAM353678 is a human miRNA-like oligonucleotide, which targets glycogen phosphorylase (glgP, NC_004631 from 4129215 to 413 1662 (+)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi Ty2 genome, as part of an anti-bacterial host defense mechanism. glgP BINDING SITE 1 and glgP BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the glgP gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of glgP BINDING SITE 1 and glgP BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glgP, a GAM353678 bacterial target gene which is associated with Salmonella ente rica enterica serovar	A

					Typhi Ty2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella enterica enterica serovar Typhi Ty2 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glgP	Salmonella enterica enterica serovar Typhi	GAM353678 is a human miRNA-like oligonucleotide, which targets glycogen phosphorylase (glgP, NC_003198 from 4144568 to 414 7015 (+)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi genome, as part of an anti-bacterial host defense mechanism. glgP BINDING SITE 1 and glgP BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the glgP gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of glgP BINDING SITE 1 and glgP BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glgP, a GAM353678 bacterial target gene which is associated with Salmonella enterica enterica serovar Typhi infection, as part of an anti-bact erial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Sal monella enterica enterica serovar Typhi infection and associat ed clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glpC	Yersinia pestis KIM	GAM353678 is a human miRNA-like oligonucleotide, which targets sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small su bunit (glpC, NC_004088 from 454677 to 456047 (+)), a bac terial target gene encoded by the Yersinia pestis KIM genome, as part of an anti-bacterial host defense mechanism. glpC BINDING SITE 1 and glpC BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the glpC gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of glpC BINDING SITE 1 and glpC BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glpC, a GAM353678 bacterial target gene which is associated with Yersinia pestis KIM infection, as part of an anti-bacterial host defense mech anism. Accordingly, the utilities of GAM353678 include the dia gnosis, prevention and treatment of Yersinia pestis KIM infect ion and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glpC	Yersinia pestis	GAM353678 is a human miRNA-like oligonucleotide, which targets anaerobic glycerol-3-phosphate dehydrogenase subunit	A

					C (glpC, NC_003143 from 4289650 to 4290897 (-)), a bacterial targe t gene encoded by the Yersinia pestis genome, as part of an an ti-bacterial host defense mechanism. glpC BINDING SITE 1 and glpC BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the glpC gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of glpC BINDING SITE 1 and glpC BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glpC, a GAM353678 bacterial target gene which is associated with Yersinia pestis infection, as part of an anti-bacterial host defense mechanis m. Accordingly, the utilities of GAM353678 include the diagnos is, prevention and treatment of Yersinia pestis infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	glpD	Brucella suis 1330	GAM353678 is a human miRNA-like oligonucleotide, which targets glycerol-3-phosphate dehydrogenase (glpD, NC_004310 from 2 10763 to 212274 (+)), a bacterial target gene encoded by th e Brucella suis 1330 genome, as part of an anti-bacterial host defense mechanism. glpD BINDING SITE 1 and glpD BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the glpD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of glpD BINDING SITE 1 and glpD BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glpD, a GAM353678 bacterial target gene which is associated with Brucella suis 1 330 infection, as part of an anti-bacterial host defense mecha nism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Brucella suis 1330 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	ipaH_5	Shigella flexneri 2a str. 2457T	GAM353678 is a human miRNA-like oligonucleotide, which targets invasion plasmid antigen (ipaH_5, NC_004741 from 2023205 to 2024848 (+)), a bacterial target gene encoded by the Shigel la flexneri 2a str. 2457T genome, as part of an anti-bacterial host defense mechanism. ipaH_5 BINDING SITE 1 and ipaH_5 BINDING SITE 2 are bacterial target binding sites that are found in the untranslated region s of mRNA encoded by the ipaH_5 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDI NG SITE III of Fig. 1. The nucleotide sequences of ipaH_5 BIND ING SITE 1 and ipaH_5 BINDING SITE 2, and the	A

					complementary se condary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ipaH_5, a GAM35367 8 bacterial target gene which is associated with Shigella flex neri 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 i nclude the diagnosis, prevention and treatment of Shigella fle xneri 2a str. 2457T infection and associated clinical conditio ns	
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	ipaH9 .8	Shigella flexneri 2a str. 3 01	GAM353678 is a human miRNA-like oligonucleotide, which targets invasion plasmid antigen (ipaH9.8, NC_004337 from 1422064 t o 1423779 (-)), a bacterial target gene encoded by the Shige lla flexneri 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. ipaH9.8 BINDING SITE 1 and ipaH9.8 BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regi ons of mRNA encoded by the ipaH9.8 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BI NDING SITE III of Fig. 1. The nucleotide sequences of ipaH9.8 BINDING SITE 1 and ipaH9.8 BINDING SITE 2, and the complementa ry secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ipaH9.8, a GAM3536 78 bacterial target gene which is associated with Shigella fle xneri 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 in clude the diagnosis, prevention and treatment of Shigella flex neri 2a str. 301 infection and associated clinical conditions.	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	livH	Bordetell a pertuss is	GAM353678 is a human miRNA-like oligonucleotide, which targets high-affinity branched-chain amino acid transport system perm ease protein (livH, NC_002929 from 1144729 to 1145607 (+)) , a bacterial target gene encoded by the Bordetella pertussis genome, as part of an anti-bacterial host defense mechanism. livH BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region of mRNA encoded by th e livH gene, corresponding to a target binding site such as BI NDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. T he nucleotide sequences of livH BINDING SITE, and the compleme ntary secondary structure to the nucleotide sequence of GAM353 678 RNA are set forth in Tables 6-7, hereby incorporated herei n. Another function of GAM353678 is to inhibit livH, a GAM353678 bacterial target gene which is associated with Bordetella pert ussis infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the di agnosis, prevention and	A

					treatment of Bordetella pertussis infe ction and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	lppI	Mycobacterium tuberculosis H37Rv	GAM353678 is a human miRNA-like oligonucleotide, which targets lppI (lppI, NC_000962 from 2291267 to 2291923 (+)), a bac terial target gene encoded by the Mycobacterium tuberculosis H 37Rv genome, as part of an anti-bacterial host defense mechani sm. lppI BINDING SITE 1 and lppI BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the lppI gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of lppI BINDING SITE 1 and lppI BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit lppI, a GAM353678 bacterial target gene which is associated with Mycobacterium t uberculosis H37Rv infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 in clude the diagnosis, prevention and treatment of Mycobacterium tuberculosis H37Rv infection and associated clinical conditio ns	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	lppI	Mycobacterium bovis subsp bovis AF2122/97	GAM353678 is a human miRNA-like oligonucleotide, which targets Probable lipoprotein lppI (lppI, NC_002945 from 2275182 to 2275838 (+)), a bacterial target gene encoded by the Mycobac terium bovis subsp bovis AF2122/97 genome, as part of an anti- bacterial host defense mechanism. lppI BINDING SITE 1 and lppI BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the lppI gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of lppI BINDING SITE 1 and lppI BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit lppI, a GAM353678 bacterial target gene which is associated with Mycobacterium bovis subsp bovis AF2122/97 infection, as part of an anti-bacte rial host defense mechanism. Accordingly, the utilities of GAM 353678 include the diagnosis, prevention and treatment of Myco bacterium bovis subsp bovis AF2122/97 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	MGAT5	Human	GAM353678 is a human miRNA-like oligonucleotide, which targets a human mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl- glucosaminyltransferase (MGAT5, Accession number: NM_002410) a s part of a host response mechanism associated with a Salmonel la typhimurium LT2 infection. MGAT5 BINDING SITE is a human target binding site that is a fo und	A

					in the the 3' untranslated region of mRNA encoded by the M GAT5 gene, corresponding to a target binding site such as BIND ING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. Add itionally, using the binding site prediction system of the pre sent invention GAM353678-A binds to sequences on orthologous UTR of rat(NM_023095). The nucleotide sequences of MGAT5 BINDIN G SITE, and the complementary secondary structure to the nucle otide sequence of GAM353678 RNA are set forth in Tables 6-7, h ereby incorporated herein. Another function of GAM353678 is to inhibit MGAT5, a GAM353678 human target gene which encodes an enzyme that catalyzes beta 1-6 branching on N-linked carbohydrates. MGAT5 is associated with Salmonella typhimurium LT2 infection, and therefore GAM35 3678 is associated with the abovementioned infection, as part of a host response mechanism. Accordingly, the utilities of GA M353678 include the diagnosis, prevention and treatment of Sal monella typhimurium LT2 infection and associated clinical cond itions. The function of MGAT5 and its association with various diseases and clinical conditions has been established by previous stu dies, as described hereinabove with reference to GAM3451.	
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	miaA	Chlamydia trachoma tis	GAM353678 is a human miRNA-like oligonucleotide, which targets tRNA isopentenylpyrophosphate transferase (miaA, NC_000117 from 899276 to 900295 (+)), a bacterial target gene encode d by the Chlamydia trachomatis genome, as part of an anti-bact erial host defense mechanism. miaA BINDING SITE 1 and miaA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the miaA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of miaA BINDING SITE 1 and miaA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit miaA, a GAM353678 bacterial target gene which is associated with Chlamydia trach omatis infection, as part of an anti-bacterial host defense me chanism. Accordingly, the utilities of GAM353678 include the d iagnosis, prevention and treatment of Chlamydia trachomatis in fection and associated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	minE	Pseudomon as putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets cell division topological specificity factor MinE (minE, NC_0 02947 from 1932680 to 1932934 (-)), a bacterial target gen e encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. minE BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region	A

					of mRNA encoded by the minE gene, corresponding to a target binding site such as BI NDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. T he nucleotide sequences of minE BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM353 678 RNA are set forth in Tables 6-7, hereby incorporated herei n. Another function of GAM353678 is to inhibit minE, a GAM353678 bacterial target gene which is associated with Pseudomonas put ida KT2440 infection, as part of an anti-bacterial host defens e mechanism. Accordingly, the utilities of GAM353678 include t he diagnosis, prevention and treatment of Pseudomonas putida K T2440 infection and associated clinical conditions	
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	nicT	Mycobacte rium tube rculosis H37Rv	GAM353678 is a human miRNA-like oligonucleotide, which targets nicT (nicT, NC_000962 from 3166681 to 3167799 (+)), a bac terial target gene encoded by the Mycobacterium tuberculosis H 37Rv genome, as part of an anti-bacterial host defense mechani sm. nicT BINDING SITE 1 and nicT BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the nicT gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of nicT BINDING SITE 1 and nicT BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit nicT, a GAM353678 bacterial target gene which is associated with Mycobacterium t uberculosis H37Rv infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium tuberculosis H37Rv infection and associated clinical conditio ns	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	nicT	Mycobacte rium bovi s subsp b ovis AF21 22/97	GAM353678 is a human miRNA-like oligonucleotide, which targets POSSIBLE NICKEL-TRANSPORT INTEGRAL MEMBRANE PROTEIN NICT (nic T, NC_002945 from 3123200 to 3124318 (+)), a bacterial tar get gene encoded by the Mycobacterium bovis subsp bovis AF2122 /97 genome, as part of an anti-bacterial host defense mechanis m. nicT BINDING SITE 1 and nicT BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the nicT gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of nicT BINDING SITE 1 and nicT BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit nicT, a GAM353678 bacterial target gene which is associated	A

					with Mycobacterium b ovis subsp bovis AF2122/97 infection, as part of an anti-bacte rial host defense mechanism. Accordingly, the utilities of GAM 353678 include the diagnosis, prevention and treatment of Myco bacterium bovis subsp bovis AF2122/97 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	nupC	Shigella flexneri 2a str. 301	GAM353678 is a human miRNA-like oligonucleotide, which targets permease of transport system for 3 nucleosides (nupC, NC_0043 37 from 2515842 to 2517083 (+)), a bacterial target gene encoded by the Shigella flexneri 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. nupC BINDING SITE 1 through nupC BINDING SITE 3 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the nupC gene, corresponding to target bi nding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of nupC BINDING SITE 1 through nupC BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA ar e set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit nupC, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 inclu de the diagnosis, prevention and treatment of Shigella flexner i 2a str. 301 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	nupC	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Nucleoside permease nupC (nupC, NC_004431 from 2795390 to 2 796631 (+)), a bacterial target gene encoded by the Escheric hia coli CFT073 genome, as part of an anti-bacterial host defe nse mechanism. nupC BINDING SITE 1 through nupC BINDING SITE 3 are bacterial target binding sites that are found in the untranslated region s of mRNA encoded by the nupC gene, corresponding to target bi nding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of nupC BINDING SITE 1 through nupC BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit nupC, a GAM353678 bacterial target gene which is associated with Escherichia coli CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	nupC	Shigella flexneri 2a str. 2	GAM353678 is a human miRNA-like oligonucleotide, which targets permease of transport system for 3 nucleosides	A

				457T	(nupC, NC_0047 41 from 2494019 to 2495221 (+)), a bacterial target gene e ncoded by the Shigella flexneri 2a str. 2457T genome, as part of an anti-bacterial host defense mechanism. nupC BINDING SITE 1 through nupC BINDING SITE 3 are bacterial target binding sites that are found in the untranslated region s of mRNA encoded by the nupC gene, corresponding to target bi nding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of nupC BINDING SITE 1 through nupC BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit nupC, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 inc lude the diagnosis, prevention and treatment of Shigella flexn eri 2a str. 2457T infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	ompG	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Outer membrane protein G precursor (ompG, NC_004431 from 16 24577 to 1625533 (+)), a bacterial target gene encoded by th e Escherichia coli CFT073 genome, as part of an anti-bacterial host defense mechanism. ompG BINDING SITE 1 and ompG BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the ompG gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of ompG BINDING SITE 1 and ompG BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ompG, a GAM353678 bacterial target gene which is associated with Escherichia coli CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	orn	Yersinia pestis	GAM353678 is a human miRNA-like oligonucleotide, which targets oligoribonuclease (orn, NC_003143 from 378331 to 378876 (+)), a bacterial target gene encoded by the Yersinia pestis genome, as part of an anti-bacterial host defense mechanism. orn BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region of mRNA encoded by the orn gene, corresponding to a target binding site such as BIND ING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of orn BINDING SITE,	A

					and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6–7, hereby incorporated herein. Another function of GAM353678 is to inhibit orn, a GAM353678 b acterial target gene which is associated with Yersinia pestis infection, as part of an anti–bacterial host defense mechanism . Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Yersinia pestis infection and associated clinical conditions	
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	oxyR	Salmonell a enteric a enteric a serovar Typhi	GAM353678 is a human miRNA–like oligonucleotide, which targets hydrogen peroxide–inducible regulon activator (oxyR, NC_00319 8 from 3607204 to 3608121 (–)), a bacterial target gene en coded by the Salmonella enterica enterica serovar Typhi genome , as part of an anti– bacterial host defense mechanism. oxyR BINDING SITE 1 and oxyR BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the oxyR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of oxyR BINDING SITE 1 and oxyR BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6–7, hereby incorporated herein. Another function of GAM353678 is to inhibit oxyR, a GAM353678 bacterial target gene which is associated with Salmonella enterica enterica serovar Typhi infection, as part of an anti–bact erial host defense mechanism. Accordingly, the utilities of GA M353678 include the diagnosis, prevention and treatment of Sal monella enterica enterica serovar Typhi infection and associat ed clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	oxyR	Salmonell a typhimu rium LT2	GAM353678 is a human miRNA–like oligonucleotide, which targets oxidative stress regulatory protein (oxyR, NC_003197 from 4343080 to 4343997 (+)), a bacterial target gene encoded by the Salmonella typhimurium LT2 genome, as part of an anti–bacte rial host defense mechanism. oxyR BINDING SITE 1 and oxyR BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the oxyR gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of oxyR BINDING SITE 1 and oxyR BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6–7, hereby incorporated herein. Another function of GAM353678 is to inhibit oxyR, a GAM353678 bacterial target gene which is associated with Salmonella typh imurium LT2 infection, as part of an anti–bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella typhimur ium LT2 infection and	A

					associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	oxyR	Salmonella enterica enterica serovar Typhi Ty2	GAM353678 is a human miRNA-like oligonucleotide, which targets hydrogen peroxide-inducible regulon activator (oxyR, NC_00463 1 from 3592864 to 3593781 (-)), a bacterial target gene en coded by the Salmonella enterica enterica serovar Typhi Ty2 genome, as part of an anti-bacterial host defense mechanism. oxyR BINDING SITE 1 and oxyR BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the oxyR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of oxyR BINDING SITE 1 and oxyR BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit oxyR, a GAM353678 bacterial target gene which is associated with Salmonella ente rica enterica serovar Typhi Ty2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities o f GAM353678 include the diagnosis, prevention and treatment of Salmonella enterica enterica serovar Typhi Ty2 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	pbpG	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets D-alanyl-D-alanine-endopeptidase (pbpG, NC_002947 from 4323 707 to 4324633 (+)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. pbpG BINDING SITE 1 and pbpG BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the pbpG gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of pbpG BINDING SITE 1 and pbpG BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit pbpG, a GAM353678 bacterial target gene which is associated with Pseudomonas put ida KT2440 infection, as part of an anti-bacterial host defens e mechanism. Accordingly, the utilities of GAM353678 include t he diagnosis, prevention and treatment of Pseudomonas putida K T2440 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	pchA	Pseudomonas aerugi nosa PA01	GAM353678 is a human miRNA-like oligonucleotide, which targets salicylate biosynthesis isochorismate synthase (pchA, NC_0025 16 from 4745120 to 4746550 (+)), a bacterial target gene e ncoded by the Pseudomonas aeruginosa PA01 genome, as part of a n anti-bacterial host defense mechanism. pchA BINDING SITE 1 and pchA BINDING SITE 2 are bacterial targ et	A

					binding sites that are found in the untranslated regions of mRNA encoded by the pchA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of pchA BINDING SITE 1 and pchA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit pchA, a GAM353678 bacterial target gene which is associated with Pseudomonas aer uginosa PA01 infection, as part of an anti-bacterial host defe nse mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas aerugi nosa PA01 infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	pcnA	Mycobacterium leprae	GAM353678 is a human miRNA-like oligonucleotide, which targets pcnA (pcnA, NC_002677 from 3248268 to 3249728 (-)), a bac terial target gene encoded by the Mycobacterium leprae genome, as part of an anti-bacterial host defense mechanism. pcnA BINDING SITE 1 and pcnA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the pcnA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of pcnA BINDING SITE 1 and pcnA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit pcnA, a GAM353678 bacterial target gene which is associated with Mycobacterium l eprae infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the di agnosis, prevention and treatment of Mycobacterium leprae infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	phnV	Salmonella enterica enterica serovar Typhi	GAM353678 is a human miRNA-like oligonucleotide, which targets probable membrane component of 2-aminoethylphosphonate transp orter (phnV, NC_003198 from 471575 to 472366 (-)), a bac terial target gene encoded by the Salmonella enterica enterica serovar Typhi genome, as part of an anti-bacterial host defen se mechanism. phnV BINDING SITE 1 and phnV BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the phnV gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of phnV BINDING SITE 1 and phnV BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit phnV, a GAM353678	A

					bacterial target gene which is associated with Salmonella ente rica enterica serovar Typhi infection, as part of an anti-bact erial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Sal monella enterica enterica serovar Typhi infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	phnV	Salmonella enterica enterica serovar Typhi Ty 2	GAM353678 is a human miRNA-like oligonucleotide, which targets probable membrane component of 2-aminoethylphosphonate transp orter (phnV, NC_004631 from 2508735 to 2509526 (+)), a bac terial target gene encoded by the Salmonella enterica enterica serovar Typhi Ty2 genome, as part of an anti-bacterial host defense mechanism. phnV BINDING SITE 1 and phnV BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the phnV gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of phnV BINDING SITE 1 and phnV BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit phnV, a GAM353678 bacterial target gene which is associated with Salmonella ente rica enterica serovar Typhi Ty2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities o f GAM353678 include the diagnosis, prevention and treatment of Salmonella enterica enterica serovar Typhi Ty2 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	phoY2	Mycobacterium bovis subsp bovis AF2122/97	GAM353678 is a human miRNA-like oligonucleotide, which targets PROBABLE PHOSPHATE-TRANSPORT SYSTEM TRANSCRIPTIONAL REGULATOR Y PROTEIN PHOY2 (phoY2, NC_002945 from 914388 to 915029 (-)), a bacterial target gene encoded by the Mycobacterium bov is subsp bovis AF2122/97 genome, as part of an anti-bacterial host defense mechanism. phoY2 BINDING SITE 1 and phoY2 BINDING SITE 2 are bacterial ta rget binding sites that are found in the untranslated regions of mRNA encoded by the phoY2 gene, corresponding to target bin ding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of phoY2 BINDING SITE 1 and phoY2 BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are s et forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit phoY2, a GAM353678 bacterial target gene which is associated with Mycobacterium bovis subsp bovis AF2122/97 infection, as part of an anti-bact erial host defense mechanism. Accordingly, the utilities of GA M353678 include the diagnosis, prevention and treatment of Myc obacterium bovis subsp bovis AF2122/97 infection and associated	A

					clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	phoY2	Mycobacterium tuberculosis H37Rv	GAM353678 is a human miRNA-like oligonucleotide, which targets phoY2 (phoY2, NC_000962 from 913556 to 914197 (-)), a b acterial target gene encoded by the Mycobacterium tuberculosis H37Rv genome, as part of an anti-bacterial host defense mecha nism. phoY2 BINDING SITE 1 and phoY2 BINDING SITE 2 are bacterial ta rget binding sites that are found in the untranslated regions of mRNA encoded by the phoY2 gene, corresponding to target bin ding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of phoY2 BINDING SITE 1 and phoY2 BINDING SITE 2, and the complementary seconda ry structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit phoY2, a GAM353678 bacterial target gene which is associated with Mycobacterium tuberculosis H37Rv infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium tuberculosis H37Rv infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	pilT	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets type IV pili twitching motility protein PilT (pilT, NC_002947 from 5816934 to 5817944 (-)), a bacterial target gene enc oded by the Pseudomonas putida KT2440 genome, as part of an an ti-bacterial host defense mechanism. pilT BINDING SITE 1 through pilT BINDING SITE 3 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the pilT gene, corresponding to target bi nding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of pilT BINDING SITE 1 through pilT BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit pilT, a GAM353678 bacterial target gene which is associated with Pseudomonas put ida KT2440 infection, as part of an anti-bacterial host defens e mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida K T2440 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	polA	Mycobacterium leprae	GAM353678 is a human miRNA-like oligonucleotide, which targets DNA polymerase I (polA, NC_002677 from 1648220 to 1650955 (-)), a bacterial target gene encoded by the Mycobacterium le prae genome, as part of an anti-bacterial host defense mechani sm. polA BINDING SITE 1 and polA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the polA gene, corresponding to target bindin g sites such as BINDING SITE I,	A

					BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of polA BINDING SITE 1 and polA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit polA, a GAM353678 bacterial target gene which is associated with Mycobacterium l eprae infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium leprae infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	prcA	Mycobacterium leprae	GAM353678 is a human miRNA-like oligonucleotide, which targets proteasome [alpha]-type subunit 1 (prcA, NC_002677 from 1576553 to 1577350 (+)), a bacterial target gene encoded by the Mycobacterium leprae genome, as part of an anti-bacterial host defense mechanism. prcA BINDING SITE 1 and prcA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the prcA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of prcA BINDING SITE 1 and prcA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit prcA, a GAM353678 bacterial target gene which is associated with Mycobacterium l eprae infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium leprae infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	pta	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets phosphate acetyltransferase (pta, NC_002947 from 891625 to 893712 (-)), a bacterial target gene encoded by the Pseudo monas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. pta BINDING SITE 1 and pta BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the pta gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of pta BINDING SITE 1 and pta BINDING SITE 2, and the complementary secondary structu re to the nucleotide sequence of GAM353678 RNA are set forth i n Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit pta, a GAM353678 b acterial target gene which is associated with Pseudomonas puti da KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis,	A

					prevention and treatment of Pseudomonas putida KT 2440 infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	ptsH	Salmonella enterica enterica serovar Typhi	GAM353678 is a human miRNA-like oligonucleotide, which targets phosphocarrier protein HPr (ptsH, NC_003198 from 2505403 to 2505660 (+)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi genome, as part of an anti-bacterial host defense mechanism. ptsH BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region of mRNA encoded by the ptsH gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. T he nucleotide sequences of ptsH BINDING SITE, and the compleme ntary secondary structure to the nucleotide sequence of GAM353 678 RNA are set forth in Tables 6-7, hereby incorporated herei n. Another function of GAM353678 is to inhibit ptsH, a GAM353678 bacterial target gene which is associated with Salmonella ente rica enterica serovar Typhi infection, as part of an anti-bact erial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Sal monella enterica enterica serovar Typhi infection and associat ed clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	rbsR	Shigella flexneri 2a str. 301	GAM353678 is a human miRNA-like oligonucleotide, which targets regulator for rbs operon (rbsR, NC_004337 from 3947708 to 3 948700 (+)), a bacterial target gene encoded by the Shigella flexneri 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. rbsR BINDING SITE 1 through rbsR BINDING SITE 3 are bacterial target binding sites that are found in the untranslated region s of mRNA encoded by the rbsR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of rbsR BINDING SITE 1 through rbsR BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA ar e set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit rbsR, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 301 infection, as part of an anti-bacterial host de fense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Shigella flexner i 2a str. 301 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	rbsR	Shigella flexneri 2a str. 2457T	GAM353678 is a human miRNA-like oligonucleotide, which targets regulator for rbs operon (rbsR, NC_004741 from 3824594 to 3 825577 (-)), a bacterial target gene encoded by the Shigella flexneri 2a str. 2457T genome, as part of an anti-bacterial h ost defense mechanism. rbsR BINDING SITE 1 through rbsR BINDING SITE 3 are bacterial target binding sites	A

					that are found in the untranslated region s of mRNA encoded by the rbsR gene, corresponding to target bi nding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of rbsR BINDING SITE 1 through rbsR BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA ar e set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit rbsR, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Shigella flexn eri 2a str. 2457T infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	rbsR	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Ribose operon repressor (rbsR, NC_004431 from 4439260 to 44 40252 (+)), a bacterial target gene encoded by the Escherich ia coli CFT073 genome, as part of an anti-bacterial host defense mechanism. rbsR BINDING SITE 1 through rbsR BINDING SITE 3 are bacterial target binding sites that are found in the untranslated region s of mRNA encoded by the rbsR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.1. The nucleotide sequences of rbsR BINDING SITE 1 through rbsR BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit rbsR, a GAM353678 bacterial target gene which is associated with Escherichia col i CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	recG	Mycobacterium leprae	GAM353678 is a human miRNA-like oligonucleotide, which targets ATP-dependent DNA helicase (recG, NC_002677 from 2014723 to 2016954 (-)), a bacterial target gene encoded by the Mycoba cterium leprae genome, as part of an anti-bacterial host defen se mechanism. recG BINDING SITE 1 and recG BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the recG gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of recG BINDING SITE 1 and recG BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit recG, a GAM353678	A

					bacterial target gene which is associated with Mycobacterium l eprae infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium leprae infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	relA	Mycobacterium bovis subsp bovis AF2122/97	GAM353678 is a human miRNA-like oligonucleotide, which targets PROBABLE GTP PYROPHOSPHOKINASE RELA (ATP:GTP 3'-PYROPHOSPHOTR ANSFERASE) (PPGPP SYNTHETASE I) ((P)PPGPP SYNTHETASE) (GTP DIP HOSPHOKINASE) (relA, NC_002945 from 2875274 to 2877646 (-)), a bacterial target gene encoded by the Mycobacterium bovis subsp bovis AF2122/97 genome, as part of an anti-bacterial host defense mechanism. relA BINDING SITE 1 and relA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the relA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of relA BINDING SITE 1 and relA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit relA, a GAM353678 bacterial target gene which is associated with Mycobacterium bovis subsp bovis AF2122/97 infection, as part of an anti-bacte rial host defense mechanism. Accordingly, the utilities of GAM 353678 include the diagnosis, prevention and treatment of Myco bacterium bovis subsp bovis AF2122/97 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	relA	Mycobacterium tuberculosis H37Rv	GAM353678 is a human miRNA-like oligonucleotide, which targets relA (relA, NC_000962 from 2907824 to 2910196 (-)), a bac terial target gene encoded by the Mycobacterium tuberculosis H 37Rv genome, as part of an anti-bacterial host defense mechani sm. relA BINDING SITE 1 and relA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the relA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of relA BINDING SITE 1 and relA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit relA, a GAM353678 bacterial target gene which is associated with Mycobacteriumt uberculosis H37Rv infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 in clude the diagnosis, prevention and treatment of Mycobacterium tuberculosis H37Rv infection and associated clinical conditio ns	A

GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	risA	Bordetella pertussis	GAM353678 is a human miRNA-like oligonucleotide, which targets tresponse regulator protein (risA, NC_002929 from 3765257 t o 3765991 (-)), a bacterial target gene encoded by the Borde tella pertussis genome, as part of an anti-bacterial host defense mechanism. risA BINDING SITE 1 and risA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the risA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of risA BINDING SITE 1 and risA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit risA, a GAM353678 bacterial target gene which is associated with Bordetella pert ussis infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Bordetella pertussis infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	rpsT	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets ribosomal protein S20 (rpsT, NC_002947 from 707068 to 7073 46 (-)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defen se mechanism. rpsT BINDING SITE 1 and rpsT BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the rpsT gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of rpsT BINDING SITE 1 and rpsT BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit rpsT, a GAM353678 bacterial target gene which is associated with Pseudomonas put ida KT2440 infection, as part of an anti-bacterial host defens e mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida K T2440 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	ruvB	Yersinia pestis	GAM353678 is a human miRNA-like oligonucleotide, which targets Holliday junction DNA helicase (ruvB, NC_003143 from 233644 9 to 2337453 (+)), a bacterial target gene encoded by the Ye rsinia pestis genome, as part of an anti-bacterial host defens e mechanism. ruvB BINDING SITE 1 and ruvB BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the ruvB gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of ruvB	A

					BINDING SITE 1 and ruvB BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ruvB, a GAM353678 bacterial target gene which is associated with Yersinia pestis infection, as part of an anti-bacterial host defense mechanis m. Accordingly, the utilities of GAM353678 include the diagnos is, prevention and treatment of Yersinia pestis infection and associated clinical conditions	
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	ruvB	Yersinia pestis KI M	GAM353678 is a human miRNA-like oligonucleotide, which targets Holliday junction helicase subunit A (ruvB, NC_004088 from 2482031 to 2483035 (-)), a bacterial target gene encoded by the Yersinia pestis KIM genome, as part of an anti-bacterial host defense mechanism. ruvB BINDING SITE 1 and ruvB BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the ruvB gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of ruvB BINDING SITE 1 and ruvB BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ruvB, a GAM353678 bacterial target gene which is associated with Yersinia pestis KIM infection, as part of an anti-bacterial host defense mech anism. Accordingly, the utilities of GAM353678 include the dia gnosis, prevention and treatment of Yersinia pestis KIM infection and associated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	selB	Pseudomon as putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets selenocysteine-specific translation elongation factor (selB, NC_002947 from 582133 to 584055 (+)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. selB BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region of mRNA encoded by th e selB gene, corresponding to a target binding site such as BI NDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. T he nucleotide sequences of selB BINDING SITE, and the compleme ntary secondary structure to the nucleotide sequence of GAM353 678 RNA are set forth in Tables 6-7, hereby incorporated herei n. Another function of GAM353678 is to inhibit selB, a GAM353678 bacterial target gene which is associated with Pseudomonas put ida KT2440 infection, as part of an anti-bacterial host defens e mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida K T2440 infection and associated clinical	A

					conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	SERPINH1	Human	GAM353678 is a human miRNA-like oligonucleotide, which targets a human Serine proteinase inhibitor clade H (heat shock prote in 47) member 1; (SERPINH1, Accession number: NM_001235) as pa rt of a host response mechanism associated with a Escherichia coli CFT073, Streptococcus pneumoniae R6, Streptococcus pneumo niae TIGR4, Streptococcus pyogenes M1 GAS, Streptococcus pyoge nes MGAS315, Streptococcus pyogenes MGAS8232 and Streptococcus pyogenes SSI-1 infections. SERPINH1 BINDING SITE 1 and SERPINH1 BINDING SITE 2 are human target binding sites that are found in the untranslated region s of mRNA encoded by the SERPINH1 gene, corresponding to targe t binding sites such as BINDING SITE I, BINDING SITE II or BIN DING SITE III of Fig. 1. Additionally, using the binding site prediction system of the present invention GAM353678-A binds t o sequences on orthologous UTR of rat(NM_017173). The nucleoti de sequences of SERPINH1 BINDING SITE 1 and SERPINH1 BINDING S ITE 2, and the complementary secondary structure to the nucleo tide sequence of GAM353678 RNA are set forth in Tables 6-7, he reby incorporated herein. Another function of GAM353678 is to inhibit SERPINH1, a GAM353 678 human target gene which encodes a heat shock protein and s erpin, that may function as a chaperone for procollagen in the ER. SERPINH1 is associated with Escherichia coli CFT073, Stre ptococcus pneumoniae R6, Streptococcus pneumoniae TIGR4, Strep tococcus pyogenes M1 GAS, Streptococcus pyogenes MGAS315, Stre ptococcus pyogenes MGAS8232 and Streptococcus pyogenes SSI-1 i nfections, and therefore GAM353678 is associated with the abov ementioned infections, as part of a host response mechanism. A ccordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT073, Streptoco ccus pneumoniae R6, Streptococcus pneumoniae TIGR4, Streptococ cus pyogenes M1 GAS, Streptococcus pyogenes MGAS315, Streptoco ccus pyogenes MGAS8232 and Streptococcus pyogenes SSI-1 infect ions and associated clinical conditions. The function of SERPINH1 and its association with various dise ases and clinical conditions has been established by previous studies, as described hereinabove with reference to GAM839.	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	sitD	Shigella flexneri 2a str. 301	GAM353678 is a human miRNA-like oligonucleotide, which targets Iron transport protein, inner membrane component (sitD, NC_00 4337 from 1405360 to 1406217 (-)), a bacterial target gene encoded by the Shigella flexneri 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. sitD BINDING SITE 1 and sitD BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the sitD gene, corresponding to target	A

					bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of sitD BINDING SITE 1 and sitD BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit sitD, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 301 infection, as part of an anti-bacterial host de fense mechanism. Accordingly, the utilities of GAM353678 inclu de the diagnosis, prevention and treatment of Shigella flexner i 2a str. 301 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	sitD	Shigella flexneri 2a str. 2457T	GAM353678 is a human miRNA-like oligonucleotide, which targets Iron transport protein, inner membrane component (sitD, NC_00 4741 from 1904666 to 1905523 (+)), a bacterial target gene encoded by the Shigella flexneri 2a str. 2457T genome, as par t of an anti-bacterial host defense mechanism. sitD BINDING SITE 1 and sitD BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the sitD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of sitD BINDING SITE 1 and sitD BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit sitD, a GAM353678 bacterial target gene which is associated with Shigella flexne ri 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 inc lude the diagnosis, prevention and treatment of Shigella flexn eri 2a str. 2457T infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	speD	Salmonella enterica enterica serovar Typhi Ty 2	GAM353678 is a human miRNA-like oligonucleotide, which targets S-adenosylmethionine decarboxylase proenzyme (speD, NC_004631 from 196380 to 197174 (-)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi Ty2 gen ome, as part of an anti-bacterial host defense mechanism. speD BINDING SITE 1 and speD BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the speD gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of speD BINDING SITE 1 and speD BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit speD, a GAM353678 bacterial target gene which is associated with Salmonella ente rica enterica serovar Typhi Ty2 infection, as part of an anti-	A

					bacterial host defense mechanism. Accordingly, the utilities o f GAM353678 include the diagnosis, prevention and treatment of Salmonella enterica enterica serovar Typhi Ty2 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	speD	Salmonella enterica enterica serovar Typhi	GAM353678 is a human miRNA-like oligonucleotide, which targets S-adenosylmethionine decarboxylase proenzyme (speD, NC_003198 from 196389 to 197183 (-)), a bacterial target gene enc oded by the Salmonella enterica enterica serovar Typhi genome, as part of an anti-bacterial host defense mechanism. speD BINDING SITE 1 and speD BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the speD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of speD BINDING SITE 1 and speD BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit speD, a GAM353678 bacterial target gene which is associated with Salmonella enterica enterica serovar Typhi infection, as part of an anti-bact erial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Sal monella enterica enterica serovar Typhi infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	speD	Salmonella typhimu rium LT2	GAM353678 is a human miRNA-like oligonucleotide, which targets S-adenosylmethionine decarboxylase (speD, NC_003197 from 1 94201 to 194995 (-)), a bacterial target gene encoded by th e Salmonella typhimurium LT2 genome, as part of an anti-bacter ial host defense mechanism. speD BINDING SITE 1 and speD BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the speD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of speD BINDING SITE 1 and speD BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit speD, a GAM353678 bacterial target gene which is associated with Salmonella typh imurium LT2 infection, as part of an anti-bacterial host defen se mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella typhimurium LT2 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ssb	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets single-stranded DNA-binding protein (ssb, NC_002947 from 5 71027 to 571572 (+)), a bacterial target gene encoded by th e	A

					Pseudomonas putida KT2440 genome, as part of an anti-bacteri al host defense mechanism. ssb BINDING SITE 1 and ssb BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of m RNA encoded by the ssb gene, corresponding to target binding s ites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of ssb BINDING SITE 1 a nd ssb BINDING SITE 2, and the complementary secondary structu re to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ssb, a GAM353678 b acterial target gene which is associated with Pseudomonas puti da KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida KT 2440 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	sseB	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Protein sseB (sseB, NC_004431 from 2922456 to 2923241 (-)), a bacterial target gene encoded by the Escherichia coli CFT 073 genome, as part of an anti-bacterial host defense mechanism. sseB BINDING SITE 1 and sseB BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the sseB gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of sseB BINDING SITE 1 and sseB BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit sseB, a GAM353678 bacterial target gene which is associated with Escherichia col i CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	tcfA	Bordetella pertussis	GAM353678 is a human miRNA-like oligonucleotide, which targets tracheal colonization factor precursor (tcfA, NC_002929 from 1264436 to 1266379 (+)), a bacterial target gene encoded b y the Bordetella pertussis genome, as part of an anti-bacteria l host defense mechanism. tcfA BINDING SITE 1 and tcfA BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the tcfA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of tcfA BINDING SITE 1 and tcfA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678	A

					RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit tcfA, a GAM353678 bacterial target gene which is associated with Bordetella pert ussis infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Bordetella pertussis infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	truA	Mycobacterium leprae	GAM353678 is a human miRNA-like oligonucleotide, which targets probable pseudouridylate synthase (truA, NC_002677 from 234 3329 to 2344078 (-)), a bacterial target gene encoded by the Mycobacterium leprae genome, as part of an anti-bacterial host defense mechanism. truA BINDING SITE 1 and truA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the truA gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of truA BINDING SITE 1 and truA BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit truA, a GAM353678 bacterial target gene which is associated with Mycobacterium l eprae infection, as part of an anti-bacterial host defense mec hanism. Accordingly, the utilities of GAM353678 include the di agnosis, prevention and treatment of Mycobacterium leprae infe ction and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	truncated fmtB	Staphylococcus aureus subsp. aureus MW2	GAM353678 is a human miRNA-like oligonucleotide, which targets truncated FmtB protein (truncated fmtB, NC_003923 from 2238 083 to 2240143 (-)), a bacterial target gene encoded by the Staphylococcus aureus subsp. aureus MW2 genome, as part of an anti-bacterial host defense mechanism. truncated fmtB BINDING SITE 1 and truncated fmtB BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the truncated fmtB gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of truncated fmtB BINDING SITE 1 and truncated fmtB BINDING SITE 2, and the complementary secondary structure to t he nucleotide sequence of GAM353678 RNA are set forth in Table s 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit truncated fmtB, a GAM353678 bacterial target gene which is associated with Staph ylococcus aureus subsp. aureus MW2 infection, as part of an an ti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Staphylococcus aureus subsp. aureus MW2 infection and associated	A

					clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	uhpA	Yersinia pestis	GAM353678 is a human miRNA-like oligonucleotide, which targets two-component system response regulator (uhpA, NC_003143 from 4522790 to 4523380 (-)), a bacterial target gene encoded by the Yersinia pestis genome, as part of an anti-bacterial host defense mechanism. uhpA BINDING SITE 1 and uhpA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the uhpA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of uhpA BINDING SITE 1 and uhpA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit uhpA, a GAM353678 bacterial target gene which is associated with Yersinia pestis infection, as part of an anti-bacterial host defense mechanis m. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Yersinia pestis infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ung	Haemophilus influenzae Rd	GAM353678 is a human miRNA-like oligonucleotide, which targets uracil DNA glycosylase (ung, NC_000907 from 18676 to 1933 5 (+)), a bacterial target gene encoded by the Haemophilus influenzae Rd genome, as part of an anti-bacterial host defen se mechanism. ung BINDING SITE 1 and ung BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ung gene, corresponding to target binding s ites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of ung BINDING SITE 1 a nd ung BINDING SITE 2, and the complementary secondary structu re to the nucleotide sequence of GAM353678 RNA are set forth i n Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ung, a GAM353678 b acterial target gene which is associated with Haemophilus infl uenzae Rd infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Haemophilus influenza e Rd infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	vanB	Pseudomonas aerugi nosa PA01	GAM353678 is a human miRNA-like oligonucleotide, which targets vanillate O-demethylase oxidoreductase (vanB, NC_002516 from 5504120 to 5505073 (+)), a bacterial target gene encoded b y the Pseudomonas aeruginosa PA01 genome, as part of an anti-b acterial host defense mechanism. vanB BINDING SITE 1 and vanB BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the vanB gene, corresponding to target bindin g sites such as BINDING SITE I,	A

					BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of vanB BINDING SITE 1 and vanB BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit vanB, a GAM353678 bacterial target gene which is associated with Pseudomonas aer uginosa PA01 infection, as part of an anti-bacterial host defe nse mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas aerugi nosa PA01 infection and associated clinical conditions	
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	yabO	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Ribosomal large subunit pseudouridine synthase A (yabO, NC_00 4431 from 61489 to 62148 (-)), a bacterial target gene encoded by the Escherichia coli CFT073 genome, as part of an anti-bacterial host defense mechanism. yabO BINDING SITE 1 and yabO BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the yabO gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of yabO BINDING SITE 1 and yabO BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit yabO, a GAM353678 bacterial target gene which is associated with Escherichia col i CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions	A
GAM353678	CAGCAGCACACTGTGGTTTGTA	Human	yciE	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Protein yciE (yciE, NC_004431 from 1558641 to 1559147 (-)), a bacterial target gene encoded by the Escherichia coli CFT 073 genome, as part of an anti-bacterial host defense mechanis m. yciE BINDING SITE 1 and yciE BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the yciE gene, corresponding to target bindin g sites such as BINDING SITE I, BINDING SITE II or BINDING SIT E III of Fig. 1. The nucleotide sequences of yciE BINDING SITE 1 and yciE BINDING SITE 2, and the complementary secondary st ructure to the nucleotide sequence of GAM353678 RNA are set fo rth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit yciE, a GAM353678 bacterial target gene which is associated with Escherichia col i CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis,	A

prevention and treatment of Escherichia coli CFT07 3 infection and associated clinical conditions

Replace paragraph 0160 with the following paragraph.

Studies documenting the well known correlations between each of a plurality of GAM TARGET GENEs that are described by Fig.1 and the known gene functions and related diseases are listed in Table 9, hereby incorporated herein. Specifically, in Table 9, lines 6046-6059 describes references of GAM target genes, as set forth in SEQ ID NO:348 in Table 8.

After paragraph 0160, add the following Table 9, paragraph, Table 11, paragraph, Table 12, paragraph, and Table 13.

Table 9:

TARGET	TARGET ORGANISM	REFERENCES
MGAT5	Human	Demetriou, M.; Granovsky, M.; Quaggin, S.; Dennis, J. W.: Negative regulation of T-cell activation and autoimmunity by Mgat5 N-glycosylation. Nature 409: 733-739, 2001.
MGAT5	Human	Granovsky, M.; Fata, J.; Pawling, J.; Muller, W. J.; Khokha, R.; Dennis, J. W.:Suppression of tumor growth and metastasis in Mgat5-deficient mice. Nature Med.6: 306-12, 2000.
MGAT5	Human	Saito, H.; Nishikawa, A.; Gu, J.; Ihara, Y.; Soejima, H.; Wada, Y.;Sekiya, C.;Niikawa, N.; Taniguchi, N.: cDNA cloning and chromosomal mapping of human N-acetyl glucosaminyltransferase V+. Biochem. Biophys. Res. Commun. 198: 318-327,1994.

Table 11, lines 275482-275565, shows data of GAM RNA SEQ ID NO:348 printed on microarray chip probes, as described in detail in Fig.17.

Table 11

PROBE SEQUENCE	PROBE TYPE	GAM RNA SEQ ID/ GAM RNA/MIR SEQUENCE MIR NAME		LIB RARY	SIG NAL	BACKG ROUND Z-SCO RE	MISM ATCH Z-SCO RE
CCCAGCAGCAC ACTGTGGTTTG TACGCGATCCG TTATCGTTCGG TATCGAACGTA ACGAT	Predicted	348	CAGCAGCACACTGTGGTTTGTA	A2	638	4.2	3.2
CCCAGCAGCAC	Predicted	348	CAGCAGCACACTGTGGTTTGTA	D2	9435	16.6	20.9

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ACTGTGGTTTG
TACGCGATCCG
TTATCGTTCGG
TATCGAACGTA
ACGAT

CCCAGCAGCAC Predicted    348    CAGCAGCACACTGTGGTTTGTA      E1  25910  14.8   27.5
ACTGTGGTTTG
TACGCGATCCG
TTATCGTTCGG
TATCGAACGTA
ACGAT

CCCAGCAGCAC Predicted    348   CAGCAGCACACTGTGGTTTGTA   F1     65518  12.0    30.2
ACTGTGGTTTG
TACGCGATCCG
TTATCGTTCGG
TATCGAACGTA
ACGAT

CCCAGCAGCAC Predicted    348   CAGCAGCACACTGTGGTTTGTA   G1     65518  10.1    29.3
ACTGTGGTTTG
TACGCGATCCG
TTATCGTTCGG
TATCGAACGTA
ACGAT

CCCAGCAGCAC Predicted    348   CAGCAGCACACTGTGGTTTGTA   H1     37067  9.9     28.2
ACTGTGGTTTG
TACGCGATCCG
TTATCGTTCGG
TATCGAACGTA
ACGAT

CCCAGCAGCAC Predicted    348   CAGCAGCACACTGTGGTTTGTA   A2     606    3.7     3.2
ACTGTGGTTTG
TACGGATCGTT
ATAACGATCCG
GTATCGAACGT
AACGA

CCCAGCAGCAC Predicted    348   CAGCAGCACACTGTGGTTTGTA   D2     7549   15.4   19.5
ACTGTGGTTTG
TACGGATCGTT
ATAACGATCCG
GTATCGAACGT
AACGA

CCCAGCAGCAC Predicted    348   CAGCAGCACACTGTGGTTTGTA   E1     20239  13.8   25.3
ACTGTGGTTTG
TACGGATCGTT
ATAACGATCCG
GTATCGAACGT
AACGA

CCCAGCAGCAC Predicted    348    CAGCAGCACACTGTGGTTTGTA   F1     65518  12.0   29.3
ACTGTGGTTTG
TACGGATCGTT
ATAACGATCCG
GTATCGAACGT
AACGA

CCCAGCAGCAC Predicted     348   CAGCAGCACACTGTGGTTTGTA   G1     65518  10.1   28.0
ACTGTGGTTTG
TACGGATCGTT
ATAACGATCCG
GTATCGAACGT
AACGA

CCCAGCAGCAC Predicted     348   CAGCAGCACACTGTGGTTTGTA   H1     27597  9.2     25.8
ACTGTGGTTTG
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TACGGATCGTT
ATAACGATCCG
GTATCGAACGT
AACGA

Table 12, line 177, shows data relating to GAM RNA SEQ ID NO:348 that were validated by means of Wet Laboratory.

Table 12

GAM RNA SEQUENCE	VALIDATION METHOD	SIGNAL	BACKGROUND Z-SCORE	MISMATCH Z-SCORE	GAM RNA SEQ-ID
CAGCAGCACACTGTGGTTTGTA	Chip strong	65518	16.623587	30.172779	348

Table 13, lines 3-42, 47-69, 84-121, 143-179, 187-207, 210-256, 264-478 shows sequence data of GAMs associated with different bacterial infections.

Table 13

ROW#	INFECTION NAME	SEQ ID NOs OF GAMS ASSOCIATED WITH INFECTION
2	Bordetella pertussis	1, 6, 10, 11, 12, 13, 16, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28,29, 33,34, 37, 41, 42, 43, 44, 47, 48, 49, 50, 52, 53, 54, 55, 57, 58, 59, 60, 63, 65,66, 67, 68, 69, 70, 71, 75, 76, 77, 79, 84, 86, 87, 88, 89, 91,94, 96, 97, 99,100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112, 113, 114, 115,117, 119, 120, 121, 122, 123, 125, 126, 127, 130, 131, 132, 133, 137, 138, 139,140, 141, 142, 145, 147, 149, 150, 151, 154, 155, 156, 157, 158, 160, 161, 162,164, 165, 166, 167, 168, 170, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181,183, 184, 185, 188, 191, 195, 196, 197, 204, 205, 211, 212, 214, 215, 216, 219,220, 222, 225, 228, 230, 231, 233, 237, 239, 241, 242, 243, 244, 250, 251, 253,262, 264, 265, 266, 268, 271, 272, 274, 276, 277, 280, 281, 282, 284, 285, 287,288, 289, 290, 293, 294, 296, 297, 299, 300, 301, 302, 304, 306, 308, 310, 312,317, 318, 321, 322, 324, 326, 327, 329, 330, 332, 333, 334, 335, 336, 339, 340,342, 343, 345, 348, 349, 350, 351, 352, 353, 355, 356, 357, 358, 360, 361, 362,364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 378, 380, 381,382, 383, 384, 385 and 49788-55666.
3	Brucella 1330 suis	1, 6, 10, 11, 12, 13, 14, 16, 18, 19, 21, 23, 27, 32, 35, 37, 39, 40, 42, 47,48, 49, 50, 52, 53, 58, 62, 63, 65, 68, 70, 71, 77, 79, 80, 85, 86 ,89, 90, 98, 102, 105, 107, 108, 109, 111, 112, 114, 115, 119, 120, 124, 125, 121, 122, 123, 126, 132, 138, 141, 142, 143, 150, 151, 152, 154, 155, 156, 157, 158, 160, 161,162, 164, 166, 168, 171, 172, 173, 175, 176, 177, 180, 181, 183, 185, 186, 190,195, 198, 199, 200, 201, 205, 207, 211, 212, 214, 215, 217, 218, 219, 220, 221,222, 225, 229, 230, 231, 233, 236, 237, 240, 241, 243, 244, 250, 251, 256, 258, 263, 264, 265, 266, 270, 277, 279, 280, 281, 282, 285, 287, 289, 290, 293, 294,295, 297, 300, 302, 303, 306, 308, 310, 312, 315, 318, 319, 320, 321, 330, 331,333, 334, 335, 342, 343, 347, 348, 349, 353, 354, 356, 357, 360, 361, 364, 365,366, 368, 369, 370, 371, 373, 374, 375, 377, 381, 382, 384 and 55667-60259.
4	Chlamydia Trachomatis	2, 3, 4, 6, 7, 8, 9, 10, 13, 14, 16, 18, 19, 20, 21, 22, 25, 26, 27, 30, 31, 32, 33, 36, 37, 38, 40, 45, 46, 47, 48, 49, 51, 52, 55, 62, 63, 64, 67, 73, 74, 75,78, 81, 82, 84, 85, 86, 87, 88, 91, 94, 95, 98, 99, 104, 105, 106, 111, 113, 116, 122, 124, 126, 128, 132, 133, 136, 138, 146, 148, 149, 152, 154, 155, 156, 157, 160, 164, 166, 167, 177, 179, 180, 181, 187, 188, 190, 192, 194, 198, 199,200, 205, 207, 208, 209, 210, 211, 213, 214, 217,

		218, 222, 224, 225, 226, 229,232, 233, 235, 236, 239, 241, 242, 243, 244, 245,248, 251, 252, 253, 254, 256,257, 259, 262, 264, 265, 269, 270, 271, 272, 273, 274, 278, 279, 287, 288, 289, 293, 295, 296, 297, 298, 299, 302, 303, 305, 306, 309, 311, 312, 316, 318, 319,320, 322, 323, 324, 325, 326, 327, 328, 330, 332, 333, 335, 338, 340, 341, 343,344, 345, 348, 349, 350, 353, 354, 356, 363, 373, 384 and 60260-67437.
6	Chlamydophila pneumoniae CWL029	3, 5, 6, 8, 9, 10, 13, 17, 20, 21, 22, 23, 25, 27, 28, 31, 32, 33, 37, 39, 45,46, 47, 48, 50, 52, 55, 62, 63, 64, 66, 67, 69, 73, 74, 82, 84, 85, 88, 89, 90,91, 92, 95, 101, 102, 104, 105, 111, 114, 124148, 125, 126, 128, 143, 146, 152, 159, 160, 161, 164, 165, 166, 168, 175180, 181, 187,176, 177, 178, 179,189, 190, 192, 194, 201, 203, 205, 207, 208,209, 212, 213, 214, 217, 218, 221,223, 224, 227, 232, 233, 234, 236, 238, 239, 241, 242, 243, 244, 245, 247, 248,252, 257, 258, 259, 260, 262, 263, 271, 272, 274, 275, 279, 281, 282, 283, 286, 289, 295, 297, 298, 299, 302, 305, 306, 309, 311, 312, 314, 319, 323, 324, 325,326, 327, 330, 333, 338, 340, 343, 344, 345, 346, 348, 349, 350, 352, 353, 354,356, 363, 377, 382, 383, 384 and 68148-75439.
7	Chlamydophila pneumoniae J138	3, 5, 6, 8, 9, 10, 17, 20, 21, 22, 23, 25, 27, 31, 32, 33, 37, 39, 45, 46, 47,50, 52, 55, 62, 63, 64, 66, 67, 69, 73, 74, 8290, 92, 95, 101,84, 85, 88, 89,102, 104, 105, 111, 114, 125, 126, 128, 148, 152, 159, 160, 161, 143, 146,164,165, 166, 168, 175, 176, 177, 178, 179, 187, 189, 190, 192, 194, 201, 203, 205, 207, 208, 209, 212, 180, 181, 213, 214, 217, 218, 221, 223, 224, 227, 232, 233, 234, 236, 238, 239, 241, 242, 243, 244, 245, 247, 248, 252, 257, 259 , 260, 262,263, 271, 272, 274, 275, 279, 281, 282, 283, 286, 289, 295, 297, 298, 299, 302,305, 306, 309, 311, 312, 314, 319, 323, 325, 326, 327, 330, 333, 338, 340, 343,344, 345, 346, 348, 349, 350, 352, 353, 354, 356, 363, 377, 382, 383, 384 and 75440-82241.
10	Escherichia coli CFT 073	1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 21, 22, 23, 25, 26,27, 28, 30, 31, 33, 34, 35, 36, 37, 39, 40, 42, 43, 45, 46, 47,48, 49, 50,51,52, 53, 55, 56, 57, 58, 59, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 75,76, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96,97, 99, 100, 101, 102, 103, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114,115, 116, 119, 120, 121, 122, 123, 124, 125, 126, 129, 131, 132, 133, 135, 136,137, 138, 140, 141, 142, 143, 145, 146, 147, 148, 152, 154, 155, 156, 157, 158,160, 161, 162, 163, 164, 165, 166, 167, 168, 171, 173, 174, 175, 176, 177, 179,180, 181, 182, 184, 185, 186, 190, 191, 192, 193, 195, 196, 197, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 220, 221, 222,223, 224, 225, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 241, 242,243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258,260, 261, 262, 265, 266, 267, 268, 270, 271, 272, 274, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 299, 300, 301, 302, 303, 305, 306, 307, 308, 309, 310, 311, 312, 314, 315, 316,317, 318, 321, 322, 323, 324, 325, 326, 327, 329, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 343, 344, 345, 347, 348, 349, 350, 351, 352, 353, 354, 355,356, 357, 358, 359, 360, 361, 364, 365, 367, 368, 369, 370, 372, 373, 374, 375,376, 378, 380, 381, 382, 383, 384, 385 and 90623-103607.
11	Haemophilus influenzae Rd	2, 3, 5, 6, 7, 8, 9, 10, 13, 15, 19, 20, 21, 22, 25, 26, 27, 30, 31, 32, 33, 34, 37, 38, 40, 41, 45, 46, 48, 49, 50, 51, 52, 66, 67, 68, 73, 53, 55, 62, 63, 64, 78, 81, 83, 84, 85, 88, 90, 91, 92, 98, 101, 105, 106, 111, 116, 117, 119, 122,123, 124, 125, 126, 134, 138, 144, 146, 149, 151, 152, 155, 156, 160, 161, 164, 165, 166, 169, 171, 172, 174, 176, 177, 179, 180, 183, 190, 197, 198, 199, 200,201, 203, 205, 207, 208, 211, 213, 214, 218, 221, 223, 226, 228, 229, 234, 236,239, 240, 242, 244, 247, 248, 251, 254, 255, 256, 259, 262, 263, 264, 271, 272,274, 277, 279, 281, 282, 283, 295, 296, 299, 302, 305, 306, 308, 311, 312, 313, 316, 317, 318, 319, 322, 323, 324, 325, 326, 327, 329, 333, 335, 338, 339, 340,343, 344, 345, 348, 351, 353, 354, 356, 365,

		368, 371, 375, 377, 379, 380, 385 and 103608-111433.
12	Leptospira interrogans serovar lai str. 56601	1, 3, 5, 7, 8, 10, 13, 19, 22, 25, 32, 38, 39, 41, 48, 49, 52, 67, 71, 73, 84,85, 90, 91, 93, 95, 117, 124, 128, 164, 174, 192, 193, 203, 178, 179, 187, 190, 207, 225, 226, 227, 229, 238, 244, 258, 259, 262, 272, 279, 193, 203, 256, 257, 295, 298, 299, 303, 306, 307, 316, 324, 327, 333, 338, 340, 344, 348 , 376, 379, 384 and 111434-116384.
15	Mycobacterium bovis AF2122/9 subsp bovis 7	1, 3, 4, 5, 6, 7, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 31, 32, 33, 36, 37, 39, 41, 42, 52, 43, 45, 46, 47, 48, 50, 51, 53, 54, 55, 57, 58, 59, 73, 75, 76, 60, 61, 62, 71,64, 65, 66, 67, 68, 69, 70, 77, 78, 79, 80, 83, 84, 86, 87, 88, 89, 100, 101, 102,90, 91, 93, 96, 97, 99, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118,119, 120, 121, 122, 123, 125, 127,130, 131, 132, 133, 134, 135, 137, 138, 139,141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 165, 166, 167, 168, 170, 171, 172, 173, 174, 175,176, 177, 178, 179, 180, 181, 183, 184, 185, 188, 189, 190, 191, 193, 194, 195,196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 210, 211, 212,213, 214, 215, 216, 218, 219, 220, 222, 225, 230, 231, 233, 236, 237, 239, 240, 241, 242, 243, 244, 245, 246, 250, 251, 252, 253, 254, 255, 256, 257, 261, 262,263, 264, 265, 266, 267, 268, 270, 271, 273, 276, 277, 278, 280, 281, 282, 283, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 296, 297, 299, 300, 302, 303, 304, 305, 306, 308, 310, 312, 313, 314, 315, 318, 320, 321, 322, 323, 324, 325,326, 327, 329, 330, 331, 332, 333, 334, 335, 336, 337, 341, 342, 345, 346, 347,348, 349, 350, 351, 352, 353, 355, 356, 357, 358, 360, 361, 362, 364, 365, 366, 367, 369, 370, 371, 372, 373, 374, 375, 376, 378, 380, 381, 382, 383, 384, 385 and 127919-137561.
16	Mycobacterium leprae	3, 4, 5, 6, 7, 12, 13, 14, 15, 18, 19, 21, 22, 23, 24, 26, 29, 31, 32, 33, 36, 37, 39, 41, 42, 43, 45, 46, 47, 48, 49, 50, 53, 54, 68, 69, 70, 57, 59, 62, 65,71, 73, 74, 75, 76, 78, 81, 83, 84, 86, 90, 94, 96, 98, 101, 103, 106, 107, 109,110, 111, 112, 113, 114, 115, 116, 118, 119, 120, 121, 123, 131, 133, 134, 135, 137, 142, 143, 144, 145, 146, 147, 149, 154, 156, 157, 158, 159, 161, 162, 163,165, 166, 167, 171, 172, 173, 174, 175, 176, 179, 183, 184, 185, 187, 188, 189,190, 193, 196, 197, 198, 199, 200, 201, 202, 204, 205, 206, 211, 212, 214, 215,216, 218, 219, 220, 221, 223, 224, 225, 228, 230, 231, 232, 233, 234, 235, 236, 237, 241, 242, 243, 245, 249, 250, 251, 253, 254, 256, 258, 261, 263, 265, 267,268, 269, 271, 274, 276, 277, 280, 281, 284, 288, 289, 290, 291, 293, 294, 295,296, 297, 299, 300, 301, 302, 303, 305, 306, 307, 309, 310, 311, 312, 313, 314,315, 318, 320, 321, 323, 324, 327, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 343, 345, 346, 347, 348, 349, 353, 355, 356, 357, 358, 360,361, 364, 365, 368, 369, 370, 371, 372, 374, 375, 376, 377, 378, 380, 381, 382,383 and 137562-144598.
18	Mycobacterium tuberculosis H37Rv	1, 3, 4, 5, 6, 7, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 31, 32, 33, 37, 39, 41, 42, 43, 50, 51, 52, 45, 46, 47, 48, 53, 54, 55, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 83, 84, 86, 87, 88, 89, 90, 91, 93, 94, 96, 97, 99, 100, 101, 102, 103, 104, 105, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117,118, 119, 120, 121, 122, 123, 125, 127, 130, 131, 132, 133, 134, 135, 137, 138,139, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,156, 157, 158, 159, 160, 161, 162, 163, 165, 166, 167, 168, 170, 171, 172, 173,174, 175, 176, 177, 178, 179, 180, 181, 183, 184, 185, 188, 189, 190, 191, 194,195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 210, 211,212, 213, 214, 215, 216, 218, 219, 220, 222, 225, 230, 231, 233, 234, 236, 237,239, 240, 241, 242, 243, 244, 245, 246, 250, 251, 252, 253, 254, 255, 256, 257, 261, 262, 263, 264, 265, 266, 267, 268, 270, 271, 272, 273, 274, 276, 277, 278, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 296,297, 298, 299, 300, 302, 303, 304,

		305, 306, 308, 310, 312, 313, 314, 315, 318,320, 321, 323, 324, 325, 326, 327, 329, 330, 331, 332, 333, 334, 335, 336, 337, 341, 342, 345, 346, 347, 348, 349, 350, 351, 352, 353, 355, 356, 357, 358, 360,361, 362, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 378,380, 381, 382, 383, 384, 385 and 146807-155497.
20	Neisseria meningitidis Z2491	1, 6, 7, 8, 10, 12, 15, 17, 21, 22, 26, 28, 30, 37, 39, 40, 45, 49, 52, 56, 58, 60, 62, 63, 67, 70, 76, 86, 89, 90, 91, 96, 98, 102, 103, 105, 107, 108, 109, 111, 112, 113, 114, 115, 122, 123, 124, 125, 126, 127, 133, 138, 141, 142, 143,145, 147, 148, 149, 152, 157, 158, 164, 165, 166, 170, 171, 175, 176, 178, 181, 183, 187, 189, 197, 203, 217, 218, 219, 220, 221, 222, 225, 229, 230, 231, 237,239, 243, 245, 247, 248, 251, 253, 254, 256, 257, 258, 259, 264, 265, 268, 273,281, 282, 283, 285, 287, 289, 290, 293, 294, 295, 297, 300, 302, 306, 308, 314, 315, 316, 319, 321, 322, 325, 327, 329, 332, 333, 334, 338, 340, 341, 344, 346,348, 349, 350, 351, 354, 355, 356, 365, 371, 372, 375, 376, 380, 381, 382, 384 and 155834-160603.
21	Pseudomonas aeruginosa PA01	1, 2, 6, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 33, 34, 35, 36, 37, 41, 42, 56, 43, 45, 46, 48, 49, 50, 52, 54, 55, 57, 58, 59, 60, 62, 63, 64, 76, 77, 78, 79, 81, 65, 66, 67, 68, 69, 70, 71, 73,82, 83, 84, 86, 87, 88, 89, 90, 91, 94, 95, 96, 97, 99, 100, 101, 102, 103, 105,106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 118, 119, 120, 121, 122,123, 124, 125, 126, 127, 130, 131, 134, 137, 138, 139, 140, 141, 142, 144, 147,149, 150, 151, 152, 154, 155, 156, 157, 158, 160, 161, 162, 163, 164, 165, 166,167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181, 183, 184, 185, 188, 190, 192, 193, 194, 195, 196, 197, 202, 204, 205, 208, 210, 211, 212,213, 214, 215, 216, 218, 220, 222, 225, 228, 229, 230, 231, 232, 233, 236, 237,241, 242, 243, 244, 250, 251, 253, 258, 262, 264, 265, 266, 267, 268, 270, 271, 272, 273, 274, 276, 277, 280, 281, 282, 283, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 296, 297, 298, 299, 300, 301, 302, 306, 312, 314, 318, 319, 320,321, 323, 324, 325, 327, 329, 330, 331, 333, 334, 335, 336, 339, 340, 341, 342,343, 345, 347, 348, 349, 350, 351, 352, 353, 355, 356, 357, 358, 360, 361, 362,364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 378, 380, 381,382, 383, 384 and 160604-170274.
22	Pseudomonas K putida T2440	1, 5, 7, 9, 10, 11, 12, 13, 14, 16, 18, 19, 23, 24, 25, 26, 27, 28, 29, 31, 33,34, 36, 37, 38, 39, 41, 42, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 54, 55, 57, 58, 59, 61, 64, 65, 66, 68, 69, 70, 71, 73, 76, 84, 85, 86, 88, 89, 91, 94, 98,99, 101, 102, 103, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 117, 118, 119, 120, 121, 122, 123, 125, 126, 131, 132, 133, 134, 135, 137, 138, 140,141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 166, 167, 168, 171, 172, 173, 174, 175,176, 177, 179, 180, 181, 183, 184, 185, 187, 190, 191, 193, 195, 196, 197, 202,204, 205, 207, 211, 212, 214, 215, 216, 220, 221, 222, 225, 228, 229, 230, 231, 232, 233, 234, 236, 237, 240, 241, 242, 243, 244, 248, 250, 251, 253, 255, 258,264, 265, 266, 267, 270, 271, 272, 274, 276, 277, 280, 281, 282, 283, 284, 285,287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 308, 310, 312, 313, 314, 316, 317, 318, 320, 321, 322, 323,324, 327, 329, 333, 334, 335, 336, 337, 342, 343, 345, 346, 347, 348, 349, 350,351, 352, 353, 354, 355, 356, 357, 358, 360, 361, 364, 365, 366, 367, 368, 369, 370, 371, 373, 374, 375, 376, 377, 378, 380, 381, 382, 383, 384, 385 and 170275-178543.
24	Salmonella enterica enterica serovar	1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 16, 17, 18, 19, 20, 21, 22, 23, 25, 26, 27, 28, 30, 31, 32, 33, 35, 37, 38, 39, 51, 40, 42, 43, 45, 46, 47, 48, 49, 50, 52, 55, 56, 57, 58, 59, 60, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 75,

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25	Salmonella enterica enterica serovar Typ hi Ty2	1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 25, 26, 27, 28, 30, 31, 32, 33, 35, 37, 38, 50, 39, 40, 42, 43, 45, 46, 47, 48, 49, 51, 52, 55, 56, 57, 58, 59, 69, 70, 71, 72, 73, 60, 62, 63, 64, 65, 66, 67, 68, 75, 77, 79, 80, 81, 83, 84, 85, 86, 88, 89, 90, 91, 94, 95, 98, 99, 100, 101,102, 105, 106, 107, 108, 109, 111, 112, 113, 114, 115, 116, 119, 120, 121, 122,123, 124, 125, 126, 127, 129, 131, 132, 133, 135, 136, 137, 138, 142, 143, 144,145, 146, 147, 148, 150, 152, 153, 154, 155, 156, 157, 158, 160, 161, 162, 163, 164, 165, 166, 167, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181, 182, 183,185, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 208, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 225, 226, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 250, 251, 252, 253, 254, 255, 256, 257, 260,261, 262, 263, 265, 266, 269, 270, 271, 272, 274, 276, 277, 278, 280, 281, 282,283, 284, 285, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299,300, 301, 302, 303, 304, 305, 306, 308, 311, 312, 314, 315, 318, 319, 323, 324, 325, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341,342, 343, 344, 345, 346, 347, 348, 349, 351, 352, 353, 354, 355, 356, 357, 358,360, 361, 364, 365, 366, 367, 369, 370, 371, 373, 374, 375, 376, 378, 379, 380, 381, 382, 383, 384, 385 and 190941-201927.
26	Salmonella typhimuri um LT2	1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24,25, 26, 27, 28, 29, 30, 31, 32, 33, 48, 49, 36, 37, 38, 39, 42, 43, 45, 46, 47, 50, 51, 52, 54, 55, 56, 57, 58, 59, 60, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 75, 77, 79, 82, 83, 84, 86, 88, 89, 90, 91, 94, 95, 96, 100, 101, 102,103, 104, 105, 107, 108, 109, 111, 112, 113, 114, 115, 116, 119, 120, 121, 122,123, 124, 125, 126, 127, 129, 131, 132, 133, 135, 137, 138, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 154, 155, 156, 157, 158, 160, 161, 162, 163,164, 165, 166, 167, 168, 170, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181,182, 183, 185, 187, 188, 189, 190, 192, 193, 194, 195, 196, 197, 198, 199, 200,201, 202, 203, 204, 205, 206, 207, 208, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236,237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 249, 250, 251, 252, 253,255, 256, 257, 258, 260, 261, 262, 263, 266, 267, 268, 270, 271, 272, 273, 274, 275, 276, 279, 280, 281, 282, 283, 285, 287, 288, 289, 290, 291, 292, 293, 294, 296, 297, 298, 299, 300, 302, 303, 306, 307, 308, 309, 310, 311, 312, 314, 315,317, 318, 319, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335,336, 337, 338, 340, 341, 342, 343, 344, 345, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 368, 369, 370,371, 373, 374, 375, 376, 379, 380, 381,

		382, 383, 384, 385 and 201928-215605.
27	Shigella 2a flexneri str.2457T	1, 2, 5, 6, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 21, 22, 23, 24, 25, 26, 27,28, 29, 30, 32, 33, 35, 36, 37, 50, 51, 38, 39, 40, 41, 42, 43, 46, 47, 48, 49,52, 54, 55, 56, 57, 58, 59, 62, 63, 65, 66, 67, 68, 69, 70, 71, 73, 76, 78, 80, 83, 84, 85, 86, 87, 88, 89, 90, 91, 93, 94, 95, 97, 99, 101, 102, 103, 104, 105,107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 119, 120, 121, 122, 123,124, 125, 126, 129, 131, 132, 133, 134, 135, 136, 137, 138, 139, 141, 142, 143, 145, 146, 147, 148, 149, 150, 151, 152, 154, 155, 156, 157, 158, 160, 161, 162,163, 164, 165, 166, 167, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181, 182,184, 185, 187, 190, 191, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 207, 208, 212, 213, 214, 216, 218, 220, 221, 222, 223, 224, 225, 229, 230, 231,232, 233, 234, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 250,251, 252, 253, 254, 255, 256, 257, 260, 261, 262, 263, 265, 268, 270, 271, 272, 274, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 287, 288, 289, 290, 291,292, 293, 295, 296, 297, 298, 299, 300, 301, 302, 304, 306, 307, 308, 309, 310,311, 312, 314, 315, 316, 317, 318, 320, 321, 322, 323, 324, 325, 327, 328, 329, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 343, 344, 345, 346, 347,348, 349, 350, 351, 352, 353, 354, 356, 357, 358, 359, 360, 361, 362, 364, 365,366, 367, 368, 369, 371, 373, 374, 375, 376, 379, 380, 381, 382, 383, 384, 385 and 215606-226197.
28	Shigella 2a flexneri str. 301	1, 2, 5, 6, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 33, 35, 36, 37, 52, 39, 40, 41, 42, 43, 46, 47, 48, 49, 50, 51, 54, 55, 56, 57, 58, 59, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 73, 76, 77, 78, 80, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 97, 99, 101, 102, 103,104, 105, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 119, 120, 121, 122,123, 124, 125, 126, 129, 132, 133, 134, 135, 136, 137, 138, 141, 142, 143, 144,145, 146, 147, 148, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, 160, 161,162, 163, 164, 165, 166, 167, 168, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181, 182, 184, 185, 187, 190, 191, 195, 196, 197, 198, 199, 200, 201, 202, 203,205, 207, 208, 210, 212, 213, 214, 216, 217, 218, 220, 221, 222, 223, 224, 225,229, 230, 231, 232, 233, 234, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245,247, 248, 250, 251, 252, 253, 254, 255, 256, 257, 260, 262, 263, 264, 265, 266,268, 269, 270, 271, 272, 274, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285,287, 288, 289, 290, 291, 292, 293, 295, 296, 297, 298, 299, 300, 301, 302, 304,306, 308, 309, 311, 312, 314, 315, 316, 317, 318, 320, 321, 323, 324, 325, 327,328, 329, 331, 333, 334, 335, 336, 337, 338, 339, 340, 341, 343, 344, 345, 346,347, 348, 349, 350, 351, 352, 353, 354, 356, 357, 358, 359, 360, 361, 362, 364,365, 366, 367, 368, 369, 371, 373, 374, 375, 376, 378, 379, 380, 381, 382, 383,384, 385 and 226198-237003.
29	Staphyl Ococcus Aureu s subsp . aureus Mu50	2, 5, 7, 8, 9, 10, 13, 16, 19, 22, 25, 27, 31, 32, 33, 35, 36, 38, 39, 40, 41, 45, 46, 47 , 48, 50, 51, 52, 55, 62, 63, 67, 71, 73, 81, 83, 84, 85, 90, 91, 92, 93, 95, 98, 100, 101, 105, 106, 111, 113, 116, 119, 120, 124, 131, 133, 138, 139, 146, 147, 149, 152 , 153, 156, 160, 161, 162, 165, 166, 169, 171, 172, 174, 177, 179, 180, 181, 190, 192, 203, 204, 205, 207, 208, 213, 214, 217, 218, 222,228, 231, 232, 236, 238, 240, 242, 244, 245, 247, 248, 252, 254, 256, 259, 261,262, 270, 271, 272, 274, 275, 287, 293, 294, 299, 301, 302, 305, 306, 308, 309, 311, 316, 317, 323, 324, 325, 326, 327, 332, 333, 334, 335, 337, 339, 340, 342,343, 344, 345, 346, 348, 349, 351, 353, 354, 356, 363, 365, 368, 371, 375, 379,381 and 237004-244310.
30	Staphyl ococcuss	2, 5, 7, 8, 10, 13, 16, 19, 22, 25, 27, 30, 31, 32, 33, 38, 39, 40, 41, 45, 46,47, 48, 50, 51, 52, 55,

	subsp. aureus MW2	62, 63, 67, 71, 72, 73, 78, 81, 83, 84, 90, 91, 92, 93, 95, 98, 100, 101, 105, 106, 109, 111, 113, 117, 119, 120, 124, 126, 128, 130,131, 133, 134, 138, 139, 143, 149, 152, 153, 156, 160, 161, 162, 166, 169, 171,172, 174, 177, 179, 180, 181, 182, 190, 192, 203, 204, 205, 207, 208, 213, 214,217, 218, 222, 228, 231, 232, 236, 238, 242, 244, 247, 248, 252, 254, 256, 257, 259, 261, 262, 271, 272, 274, 279, 287, 293, 294, 295, 299, 301, 302, 306, 307,308, 309, 315, 316, 323, 324, 325, 326, 327, 332, 333, 334, 335, 337, 338, 339,342, 343, 344, 345, 346, 348, 350, 351, 353, 356, 363, 365, 368, 371, 375, 379, 381 and 244311-250683.
31	Staphylococcus aureus subsp. aureus N315	2, 5, 7, 8, 9, 10, 13, 16, 19, 22, 25, 27, 31, 32, 33, 35, 36, 38, 39, 40, 41, 45, 46, 47, 48, 50, 51, 52, 55, 62, 63 , 67, 71, 73, 81, 83, 84, 85, 90, 91, 92, 93, 95, 98, 100, 101, 105, 106, 111, 113, 117, 119, 120, 124, 131, 133, 134, 138, 139, 143, 146, 147, 149, 152, 153, 156, 160, 161, 162, 166, 169, 171, 172,174, 177, 179, 180, 181, 190, 192, 203, 204, 205, 207, 208, 213, 214, 217, 218, 222, 226, 228, 231, 232, 236, 238, 240, 242, 244, 245, 247, 248, 252, 254, 256, 259, 260, 261, 262, 270, 271, 272, 274, 275, 279, 287, 293, 294, 299, 301, 302,305, 306, 307, 308, 309, 311, 316, 317, 323, 324, 325, 326, 327, 332, 333, 334,335, 337, 339, 340, 342, 343, 344, 345, 346, 348, 349, 351, 353, 354, 356, 363,365, 368, 371, 375, 379, 381 and 250684-257140.
32	Streptococcus Pneumoniae R6	2, 3, 5, 6, 10, 13, 14, 17, 20, 21, 22, 23, 25, 26, 27, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 41, 46, 47, 48, 49, 50, 52, 55, 56, 62,63, 67, 73, 77, 81, 83,84, 85, 87, 90, 91, 92, 94, 95, 100, 101, 102, 105, 106, 111, 112, 114, 115, 116, 117, 119, 123, 124, 126, 133, 136, 138, 143, 145, 146, 147, 149, 152, 156,160, 161, 164, 166, 168, 169, 171, 172, 174, 175, 176, 177, 179, 180, 190, 192, 203, 204, 205, 208, 209, 213, 214, 217, 218, 223, 226, 228, 229, 232, 233, 235, 236, 238, 239, 242, 244, 245, 246, 247, 248, 249, 252, 255, 256, 257, 258, 259, 260, 261, 262, 264, 268, 271, 272, 274, 279, 282, 283, 284, 287, 295, 296, 297, 298, 299, 300, 302, 303, 305, 306, 307, 309, 311, 312, 314, 315, 316, 320, 321, 323, 324, 325, 326, 327, 329, 333, 335, 338, 340, 341, 344, 345, 348, 350, 351, 352, 353, 356, 357, 359, 365, 368, 371, 372, 373, 375, 377, 379, 380, 382, 384,385 and 257141-265301.
33	Streptococcus pneumoniae TIGR4	2, 10, 13, 25, 27, 33, 46, 48, 50, 52, 55, 62, 63, 67, 73, 81, 84, 91, 101, 105, 106, 111, 119, 149, 152, 160, 161, 176, 177, 164, 166, 168, 169, 171, 172, 175, 179, 180, 190, 205, 208, 213, 214, 218, 228, 236, 242, 244, 246, 262, 268, 271,272, 274, 297, 299, 306, 321, 323, 324, 325, 327, 329, 333, 340, 345, 348, 351, 353, 356, 359, 365, 368, 371, 372, 375, 380 and 265302-266788.
34	Streptococcus pyogenes M1 GAS	3, 5, 8, 10, 21, 22, 25, 27, 32, 37, 38, 39, 40, 43, 49, 90, 95, 96, 106, 116,126, 129, 138, 163, 164, 168, 175, 261, 262, 176, 180, 226, 232, 244, 246, 259,268, 283, 295, 296, 297, 299, 306, 309, 316, 321, 329, 330, 333, 348, 349, 359, 372, 379, 380 and 266789-269521.
35	Streptococcus pyogenes MGAS315	3, 8, 10, 13, 20, 22, 25, 27, 31, 32, 33, 37, 38, 40, 46, 48, 52, 55, 62, 67,73, 84, 90, 91, 105, 106, 113, 116, 175, 176, 129, 138, 152, 160, 164, 166, 168,177, 179, 180, 186, 190, 192, 205, 208, 211, 213, 214, 218, 226, 229, 232, 236,242, 244, 246, 262, 268, 271, 272, 274, 282, 283, 295, 296, 297, 299, 306, 309, 312, 321, 323, 324, 325, 327, 329, 333, 340, 345, 348, 349, 353, 356, 359, 372,379, 380, 381 and 269522-272357.
36	Streptococcus pyogenes MGAS8232	3, 4, 8, 10, 13, 21, 22, 25, 27, 31, 33, 37, 38, 39, 40, 46, 48, 52, 55, 62, 67,73, 84, 90, 91, 95, 105, 106, 113, 116, 129, 138,168, 152, 160, 163, 164, 166,175, 176, 177, 179, 180, 190, 205, 208, 213, 214, 218, 226, 232, 236, 242, 244,246, 247, 259, 260, 261, 262, 268, 271, 272, 274, 295, 296, 297, 299, 306, 307,309, 316, 321, 323, 324, 325, 327, 329, 330, 333, 337, 340, 344, 345, 348, 349,353, 356, 359, 363, 372, 379, 380, 381 and 272358-275553.
37	Streptococcus	10, 13, 25, 27, 31, 33, 46, 48, 52, 55, 62, 67, 73, 84, 91,

	pyogenes SSI-1	164, 166, 168, 175, 176, 177, 179, 180, 190, 205, 208, 213, 214, 242,218, 236, 244, 246, 262, 268, 271, 272, 274, 297, 299, 306, 324, 325,327, 329, 321, 323,105, 113, 152, 160,333, 340, 345, 348, 353, 356, 359, 372, 380, 381 and 275554-276703.
38	Treponema subsp. pallidum str. Nichols	3, 10, 13, 48, 52, 57, 59, 67, 81, 84, 86, 90, 91, 121, 131, 134, 174, 175, 176, 184, 218, 228, 231, 235, 236, 243, 261, 262, 269, 272, 306, 289, 291, 295, 299, 312, 324, 329, 332, 333, 340 , 345, 356, 358 and 276704-277654.
39	Yersinia pestis	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 16, 18, 19, 21, 22, 25, 26, 27, 28, 29,30, 31, 32, 33, 34, 36, 37, 39, 40, 41, 54, 42, 43, 45, 46, 47, 48, 51, 52, 53,55, 57, 58, 61, 62, 63, 67, 68, 70, 71, 73, 75, 76, 78, 82, 84, 85, 87, 88, 89, 90, 91, 93, 94, 95, 98, 99, 101, 102, 103, 105, 106, 107, 108, 111, 112, 113, 114, 115, 116, 117, 120, 121, 122, 123, 124, 125, 126, 129, 130, 131, 132, 133, 134, 135, 136, 138, 140, 141, 142, 143, 146, 148, 149, 151, 152, 153, 154, 155, 156, 160, 164, 165, 166, 167, 169, 171, 172, 174, 175, 176, 177, 178, 179, 180, 182, 184, 186, 187, 188, 190, 191, 192, 193, 196, 197, 198, 199, 200, 201, 202, 203, 205, 206, 208, 209, 211, 213, 214, 215, 217, 218, 219, 220, 221, 222, 224, 225, 226, 227, 229, 230, 232, 233, 234, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 250, 251, 252, 253, 255, 256, 257, 258, 259, 260, 262, 263, 264, 270, 271, 272, 274, 276, 279, 280, 281, 282, 283, 286, 287, 289, 291, 292, 293, 295, 296, 298, 299, 300, 301, 302, 304, 306, 307, 308, 309, 311, 314, 315, 317, 319, 321, 322, 323, 324, 325, 326, 327, 329, 330, 331, 333, 334, 335, 336, 337, 340,341, 342, 343, 344, 345, 346, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 363, 364, 365, 367, 368, 370, 372, 373, 374, 376, 377, 378, 379, 380,381, 382, 383, 384 and 277655-287825.
40	Yersinia pestis KIM	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 16, 18, 19, 20, 21, 22, 25, 26, 27, 28,29, 31, 32, 33, 34, 36, 37, 39, 40, 41, 53, 54, 42, 43, 45, 46, 47, 48, 51, 52,55, 57, 58, 61, 62, 63, 65, 67, 68, 70, 71, 72, 73, 75, 76, 78, 84, 85, 87, 88, 89, 90, 91, 93, 94, 95, 97, 99, 101, 102, 103, 105, 106, 107, 108, 111, 112, 113, 114, 115, 117, 118, 120, 121, 122, 123, 124, 125, 126, 129, 130, 131, 132, 133, 134, 135, 136, 138, 140, 142, 143, 146, 147, 148, 149, 151, 152, 153, 154, 156, 158, 160, 164, 165, 166, 169, 171, 172, 174, 175, 176, 177, 178, 179, 180,182, 186, 187, 188, 190, 191, 192, 193, 196, 197, 198, 199, 200, 201, 202, 203, 205, 206, 207, 208, 209, 211, 213, 214, 215, 217, 218, 220, 221, 222, 224, 225, 226, 227, 229, 230, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 247, 248, 250, 251, 252, 253, 255, 256, 257, 258, 260, 262, 263, 264, 270, 271, 272, 274, 276, 279, 281, 282, 283, 284, 286, 287, 288, 289, 291, 292, 293, 294, 295, 296, 298, 299, 300, 302, 303, 305, 306, 307, 308, 309, 311, 314, 315,317, 318, 319, 321, 322, 323, 324, 325, 327, 329, 330, 331, 333, 334, 335, 336,337, 340, 341, 342, 343, 344, 345, 346, 348, 349, 350, 351, 352, 353, 354, 355,356, 357, 358, 359, 362, 363, 364, 365, 367, 368, 370, 373, 374, 375, 376, 377,378, 379, 380, 381, 382, 383, 384, 385 and 287826-298021.